PCT

WORLD INTELLECTUAL PROPERTY ORGANIZATION
International Bureau

INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification [6] : **C12N 15/11, 9/00, C07H 21/00, 19/04**	**A2**	(11) International Publication Number: **WO 99/55857** (43) International Publication Date: 4 November 1999 (04.11.99)

(21) International Application Number: PCT/US99/09348

(22) International Filing Date: 28 April 1999 (28.04.99)

(30) Priority Data:
60/083,727   29 April 1998 (29.04.98)   US
09/186,675   4 November 1998 (04.11.98)   US

(71) Applicant *(for all designated States except US)*: RIBOZYME PHARMACEUTICALS, INC. [US/US]; 2959 Wilderness Place, Boulder, CO 80301 (US).

(72) Inventors; and
(75) Inventors/Applicants *(for US only)*: BEIGELMAN, Leonid [US/US]; 5530 Colt Drive, Longmont, CO 80503 (US). BURGIN, Alex [US/US]; 832 Caminito Estrella, Chula Vista, CA 91910 (US). BEAUDRY, Amber [US/US]; 13068 Westlake Place, Broomfield, CO 80026 (US). KARPEISKY, Alexander [RU/US]; 420 Vernier Avenue, Lafayette, CO 80026 (US). MATULIC–ADAMIC, Jasenka [HR/US]; 760 South 42nd Street, Boulder, CO 80303 (US). SWEEDLER, David [US/US]; 956 St. Andrews Lane, Louisville, CO 80027 (US). ZINNEN, Shawn [US/US]; 2378 Birch Street, Denver, CO 80207 (US).

(74) Agents: WARBURG, Richard, J. et al.; Lyon & Lyon LLP, Suite 4700, 633 West Fifth Street, Los Angeles, CA 90071–2066 (US).

(81) Designated States: AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, HR, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, US, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SL, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG).

Published
Without international search report and to be republished upon receipt of that report.

---

(54) Title: NUCLEOSIDE TRIPHOSPHATES AND THEIR INCORPORATION INTO RIBOZYMES

(57) Abstract

    Novel nucleotide triphosphates, methods of synthesis and process of incorporating these nucleotide triphosphates into oligonucleotides, and isolation of novel nucleic acid catalysts (e.g., ribozymes) are disclosed.

FOR THE PURPOSES OF INFORMATION ONLY

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AL	Albania	ES	Spain	LS	Lesotho	SI	Slovenia
AM	Armenia	FI	Finland	LT	Lithuania	SK	Slovakia
AT	Austria	FR	France	LU	Luxembourg	SN	Senegal
AU	Australia	GA	Gabon	LV	Latvia	SZ	Swaziland
AZ	Azerbaijan	GB	United Kingdom	MC	Monaco	TD	Chad
BA	Bosnia and Herzegovina	GE	Georgia	MD	Republic of Moldova	TG	Togo
BB	Barbados	GH	Ghana	MG	Madagascar	TJ	Tajikistan
BE	Belgium	GN	Guinea	MK	The former Yugoslav	TM	Turkmenistan
BF	Burkina Faso	GR	Greece		Republic of Macedonia	TR	Turkey
BG	Bulgaria	HU	Hungary	ML	Mali	TT	Trinidad and Tobago
BJ	Benin	IE	Ireland	MN	Mongolia	UA	Ukraine
BR	Brazil	IL	Israel	MR	Mauritania	UG	Uganda
BY	Belarus	IS	Iceland	MW	Malawi	US	United States of America
CA	Canada	IT	Italy	MX	Mexico	UZ	Uzbekistan
CF	Central African Republic	JP	Japan	NE	Niger	VN	Viet Nam
CG	Congo	KE	Kenya	NL	Netherlands	YU	Yugoslavia
CH	Switzerland	KG	Kyrgyzstan	NO	Norway	ZW	Zimbabwe
CI	Côte d'Ivoire	KP	Democratic People's	NZ	New Zealand		
CM	Cameroon		Republic of Korea	PL	Poland		
CN	China	KR	Republic of Korea	PT	Portugal		
CU	Cuba	KZ	Kazakstan	RO	Romania		
CZ	Czech Republic	LC	Saint Lucia	RU	Russian Federation		
DE	Germany	LI	Liechtenstein	SD	Sudan		
DK	Denmark	LK	Sri Lanka	SE	Sweden		
EE	Estonia	LR	Liberia	SG	Singapore		

DESCRIPTION

NUCLEOSIDE TRIPHOSPHATES AND THEIR INCORPORATION INTO RIBOZYMES

Related Applications

5   This patent application claims priority to Beigelman et al., USSN , 09/186,675 filed November 4, 1998, Beigelman et al., USSN 60/083,727, filed April 29, 1998, and Beigelman et al., USSN 60/064,866 filed November 5, 1997, all of these earlier applications are entitled "NUCLEOTIDE TRIPHOSPHATES AND THEIR INCORPORATION INTO OLIGONUCLEOTIDES". Each of these

10   applications are hereby incorporated by reference herein in their entirety including the drawings.

Background of the Invention

This invention relates to novel nucleotide triphosphates (NTPs); methods for synthesizing nucleotide triphosphates; and methods for incorporation of novel

15   nucleotide triphosphates into oligonucleotides. The invention further relates to incorporation of these nucleotide triphosphates into nucleic acid molecules using polymerases under several novel reaction conditions.

The following is a brief description of nucleotide triphosphates. This summary is not meant to be complete, but is provided only to assist understanding of

20   the invention that follows. This summary is not an admission that all of the work described below is prior art to the claimed invention.

The synthesis of nucleotide triphosphates and their incorporation into nucleic acids using polymerase enzymes has greatly assisted in the advancement of nucleic acid research. The polymerase enzyme utilizes nucleotide triphosphates as precursor

25   molecules to assemble oligonucleotides. Each nucleotide is attached by a phosphodiester bond formed through nucleophilic attack by the 3' hydroxyl group of the oligonucleotide's last nucleotide onto the 5' triphosphate of the next nucleotide. Nucleotides are incorporated one at a time into the oligonucleotide in a 5' to 3' direction. This process allows RNA to be produced and amplified from virtually any

30   DNA or RNA templates.

2

Most natural polymerase enzymes incorporate standard nucleotide triphosphates into nucleic acid. For example, a DNA polymerase incorporates dATP, dTTP, dCTP, and dGTP into DNA and an RNA polymerase generally incorporates ATP, CTP, UTP, and GTP into RNA. There are however, certain
5   polymerases that are capable of incorporating non-standard nucleotide triphosphates into nucleic acids (Joyce, 1997, *PNAS* 94, 1619-1622, Huang et al., *Biochemistry* 36, 8231-8242).

Before nucleosides can be incorporated into RNA transcripts using polymerase enzymes they must first be converted into nucleotide triphosphates which can be
10   recognized by these enzymes. Phosphorylation of unblocked nucleosides by treatment with $POCl_3$ and trialkyl phosphates was shown to yield nucleoside 5'-phosphorodichloridates (Yoshikawa *et al.*, 1969, *Bull. Chem. Soc.(Japan)* 42, 3505). Adenosine or 2'-deoxyadenosine 5'-triphosphate was synthesized by adding an additional step consisting of treatment with excess tri-n-butylammonium
15   pyrophosphate in DMF followed by hydrolysis (Ludwig, 1981, *Acta Biochim. et Biophys. Acad. Sci. Hung.* 16, 131-133).

Non-standard nucleotide triphosphates are not readily incorporated into RNA transcripts by traditional RNA polymerases. Mutations have been introduced into RNA polymerase to facilitate incorporation of deoxyribonucleotides into RNA
20   (Sousa & Padilla, 1995, *EMBO J.* 14, 4609-4621, Bonner *et al.*, 1992, *EMBO J.* 11, 3767-3775, Bonner et al., 1994, *J. Biol. Chem.* 42, 25120-25128, Aurup *et al.*, 1992, *Biochemistry* 31, 9636-9641).

McGee *et al.*, International PCT Publication No. WO 95/35102, describes the incorporation of 2'-NH_2-NTP's, 2'-F-NTP's, and 2'-deoxy-2'-benzyloxyamino UTP
25   into RNA using bacteriophage T7 polymerase.

Wieczorek *et al.*, 1994, *Bioorganic & Medicinal Chemistry Letters* 4, 987-994, describes the incorporation of 7-deaza-adenosine triphosphate into an RNA transcript using bacteriophage T7 RNA polymerase.

Lin *et al.*, 1994, *Nucleic Acids Research* 22, 5229-5234, reports the
30   incorporation of 2'-NH_2-CTP and 2'-NH_2-UTP into RNA using bacteriophage T7 RNA polymerase and polyethylene glycol containing buffer. The article describes the use of the polymerase synthesized RNA for *in vitro* selection of aptamers to human neutrophil elastase (HNE).

Summary of the Invention

This invention relates to novel nucleotide triphosphate (NTP) molecules, and their incorporation into nucleic acid molecules, including nucleic acid catalysts. The NTPs of the instant invention are distinct from other NTPs known in the art. The invention further relates to incorporation of these nucleotide triphosphates into oligonucleotides using an RNA polymerase; the invention further relates to novel transcription conditions for the incorporation of modified (non-standard) and unmodified NTP's into nucleic acid molecules. Further, the invention relates to methods for synthesis of novel NTP's

In a first aspect, the invention features NTP's having the formula triphosphate-OR, for example the following formula I:
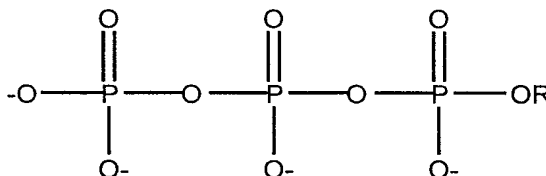
where R is any nucleoside; specifically the nucleosides 2'-O-methyl-2,6-diaminopurine riboside; 2'-deoxy-2'amino-2,6-diaminopurine riboside; 2'-(N-alanyl) amino-2'-deoxy-uridine; 2'-(N-phenylalanyl)amino-2'-deoxy-uridine; 2'-deoxy -2'-(N-β-alanyl) amino ; 2'-deoxy-2'-(lysiyl) amino uridine; 2'-C-allyl uridine; 2'-O-amino-uridine; 2'-O-methylthiomethyl adenosine; 2'-O-methylthiomethyl cytidine ; 2'-O-methylthiomethyl guanosine; 2'-O-methylthiomethyl-uridine; 2'-Deoxy-2'-(N-histidyl) amino uridine; 2'-deoxy-2'-amino-5-methyl cytidine; 2'-(N-β-carboxamidine-β-alanyl)amino-2'-deoxy-uridine; 2'-deoxy-2'-(N-β-alanyl)-guanosine; 2'-O-amino-adenosine; 2'-(N-lysyl)amino -2'-deoxy-cytidine; 2'-Deoxy -2'-(L-histidine) amino Cytidine; and 5-Imidazoleacetic acid 2'-deoxy-5'-triphosphate uridine. In a second aspect, the invention features a process for the synthesis of pyrimidine nucleotide triphosphate (such as UTP, 2'-O-MTM-UTP, dUTP and the like) including the steps of monophosphorylation where the pyrimidine nucleoside is contacted with a mixture having a phosphorylating agent (such as phosphorus oxychloride, phospho-tris-triazolides, phospho-tris-triimidazolides and the like), trialkyl phosphate (such as triethylphosphate or trimethylphosphate or the like) and dimethylaminopyridine (DMAP) under conditions suitable for the formation of pyrimidine monophosphate; and pyrophosphorylation where the pyrimidine monophosphate is contacted with a

pyrophosphorylating reagent (such as tributylammonium pyrophosphate) under conditions suitable for the formation of pyrimidine triphosphates.

The term "nucleotide" as used herein is as recognized in the art to include natural bases (standard), and modified bases well known in the art. Such bases are generally located at the 1' position of a sugar moiety. Nucleotides generally include a base, a sugar and a phosphate group. The nucleotides can be unmodified or modified at the sugar, phosphate and/or base moiety, (also referred to interchangeably as nucleotide analogs, modified nucleotides, non-natural nucleotides, non-standard nucleotides and other; see for example, Usman and McSwiggen, *supra*; Eckstein *et al.*, International PCT Publication No. WO 92/07065; Usman *et al.*, International PCT Publication No. WO 93/15187; all hereby incorporated by reference herein). There are several examples of modified nucleic acid bases known in the art as recently summarized by Limbach *et al.*, 1994, *Nucleic Acids Res.* 22, 2183. Some of the non-limiting examples of base modifications that can be introduced into nucleic acids without significantly effecting their catalytic activity include, inosine, purine, pyridin-4-one, pyridin-2-one, phenyl, pseudouracil, 2, 4, 6-trimethoxy benzene, 3-methyl uracil, dihydrouridine, naphthyl, aminophenyl, 5-alkylcytidines (*e.g.*, 5-methylcytidine), 5-alkyluridines (*e.g.*, ribothymidine), 5-halouridine (*e.g.*, 5-bromouridine) or 6-azapyrimidines or 6-alkylpyrimidines (*e.g.* 6-methyluridine) and others (Burgin *et al.*, 1996, *Biochemistry*, 35, 14090). By "modified bases" in this aspect is meant nucleotide bases other than adenine, guanine, cytosine and uracil at 1' position or their equivalents; such bases may be used within the catalytic core of an enzymatic nucleic acid molecule and/or in the substrate-binding regions of such a molecule. Such modified nucleotides include dideoxynucleotides which have pharmaceutical utility well known in the art, as well as utility in basic molecular biology methods such as sequencing.

By "unmodified nucleoside" or "unmodified nucleotide" is meant one of the bases adenine, cytosine, guanine, uracil joined to the 1' carbon of β-D-ribo-furanose.

By "modified nucleoside" or "modified nucleotide" is meant any nucleotide base which contains a modification in the chemical structure of an unmodified nucleotide base, sugar and/or phosphate.

By "pyrimidines" is meant nucleotides comprising modified or unmodified derivatives of a six membered pyrimidine ring. An example of a pyrimidine is modified or unmodified uridine.

By "nucleotide triphosphate" or "NTP" is meant a nucleoside bound to three inorganic phosphate groups at the 5' hydroxyl group of the modified or unmodified ribose or deoxyribose sugar where the 1' position of the sugar may comprise a nucleic acid base or hydrogen. The triphosphate portion may be modified to include chemical moieties which do not destroy the functionality of the group (*i.e.*, allow incorporation into an RNA molecule).

In another preferred embodiment, nucleotide triphosphates (NTPs) of the instant invention are incorporated into an oligonucleotide using an RNA polymerase enzyme. RNA polymerases include but are not limited to mutated and wild type versions of bacteriophage T7, SP6, or T3 RNA polymerases. Applicant has also found that the NTPs of the present invention can be incorporated into oligonucleotides using certain DNA polymerases, such as Taq polymerase.

In yet another preferred embodiment, the invention features a process for incorporating modified NTP's into an oligonucleotide including the step of incubating a mixture having a DNA template, RNA polymerase, NTP, and an enhancer of modified NTP incorporation under conditions suitable for the incorporation of the modified NTP into the oligonucleotide.

By "enhancer of modified NTP incorporation" is meant a reagent which facilitates the incorporation of modified nucleotides into a nucleic acid transcript by an RNA polymerase. Such reagents include but are not limited to methanol; LiCl; polyethylene glycol (PEG); diethyl ether; propanol; methyl amine; ethanol and the like.

In another preferred embodiment, the modified nucleotide triphosphates can be incorporated by transcription into a nucleic acid molecules including enzymatic nucleic acid, antisense, 2-5A antisense chimera, oligonucleotides, triplex forming oligonucleotide (TFO), aptamers and the like (Stull *et al.*, 1995 *Pharmaceutical Res.* 12, 465).

By "antisense" it is meant a non-enzymatic nucleic acid molecule that binds to target RNA by means of RNA-RNA or RNA-DNA or RNA-PNA (protein nucleic acid; Egholm *et al.*, 1993 *Nature* 365, 566) interactions and alters the activity of the

target RNA (for a review see Stein and Cheng, 1993 *Science* 261, 1004; Agrawal *et al.*, U.S. Patent No. 5,591,721; Agrawal, U.S. Patent No. 5,652,356). Typically, antisense molecules will be complementary to a target sequence along a single contiguous sequence of the antisense molecule. However, in certain embodiments, an antisense molecule may bind to substrate such that the substrate molecule forms a loop, and/or an antisense molecule may bind such that the antisense molecule forms a loop. Thus, the antisense molecule may be complementary to two (or even more) non-contiguous substrate sequences or two (or even more) non-contiguous sequence portions of an antisense molecule may be complementary to a target sequence or both.

By "2-5A antisense chimera" it is meant, an antisense oligonucleotide containing a 5' phosphorylated 2'-5'-linked adenylate residues. These chimeras bind to target RNA in a sequence-specific manner and activate a cellular 2-5A-dependent ribonuclease which, in turn, cleaves the target RNA (Torrence *et al.*, 1993 *Proc. Natl. Acad. Sci. USA* 90, 1300).

By "triplex forming oligonucleotides (TFO)" it is meant an oligonucleotide that can bind to a double-stranded DNA in a sequence-specific manner to form a triple-strand helix. Formation of such triple helix structure has been shown to inhibit transcription of the targeted gene (Duval-Valentin *et al.*, 1992 *Proc. Natl. Acad. Sci. USA* 89, 504).

By "oligonucleotide" as used herein is meant a molecule having two or more nucleotides. The polynucleotide can be single, double or multiple stranded and may have modified or unmodified nucleotides or non-nucleotides or various mixtures and combinations thereof.

By "nucleic acid catalyst" is meant a nucleic acid molecule capable of catalyzing (altering the velocity and/or rate of) a variety of reactions including the ability to repeatedly cleave other separate nucleic acid molecules (endonuclease activity) in a nucleotide base sequence-specific manner. Such a molecule with endonuclease activity may have complementarity in a substrate binding region to a specified gene target, and also has an enzymatic activity that specifically cleaves RNA or DNA in that target. That is, the nucleic acid molecule with endonuclease activity is able to intramolecularly or intermolecularly cleave RNA or DNA and thereby inactivate a target RNA or DNA molecule. This complementarity functions to allow sufficient hybridization of the enzymatic RNA molecule to the target RNA

or DNA to allow the cleavage to occur. 100% complementarity is preferred, but complementarity as low as 50-75% may also be useful in this invention. The nucleic acids may be modified at the base, sugar, and/or phosphate groups. The term enzymatic nucleic acid is used interchangeably with phrases such as ribozymes, catalytic RNA, enzymatic RNA, catalytic DNA, catalytic oligonucleotides, nucleozyme, DNAzyme, RNA enzyme, endoribonuclease, endonuclease, minizyme, leadzyme, oligozyme, finderon or DNA enzyme. All of these terminologies describe nucleic acid molecules with enzymatic activity. The specific enzymatic nucleic acid molecules described in the instant application are not limiting in the invention and those skilled in the art will recognize that all that is important in an enzymatic nucleic acid molecule of this invention is that it has a specific substrate binding site which is complementary to one or more of the target nucleic acid regions, and that it have nucleotide sequences within or surrounding that substrate binding site which impart a nucleic acid cleaving activity to the molecule (Cech et al., U.S. Patent No. 4,987,071; Cech *et al.*, 1988, 260 *JAMA* 3030).

By "enzymatic portion" or "catalytic domain" is meant that portion/region of the enzymatic nucleic acid molecule essential for cleavage of a nucleic acid substrate.

By "substrate binding arm" or "substrate binding domain" is meant that portion/region of a enzymatic nucleic acid molecule which is complementary to (*i.e.*, able to base-pair with) a portion of its substrate. Generally, such complementarity is 100%, but can be less if desired. For example, as few as 10 bases out of 14 may be base-paired. That is, these arms contain sequences within a enzymatic nucleic acid molecule which are intended to bring enzymatic nucleic acid molecule and target together through complementary base-pairing interactions. The enzymatic nucleic acid molecule of the invention may have binding arms that are contiguous or non-contiguous and may be varying lengths. The length of the binding arm(s) are preferably greater than or equal to four nucleotides; specifically 12-100 nucleotides; more specifically 14-24 nucleotides long. If two binding arms are chosen, the design is such that the length of the binding arms are symmetrical (*i.e.*, each of the binding arms is of the same length; *e.g.*, five and five nucleotides, six and six nucleotides or seven and seven nucleotides long) or asymmetrical (*i.e.*, the binding arms are of different length; *e.g.*, six and three nucleotides; three and six nucleotides long; four and five nucleotides long; four and six nucleotides long; four and seven nucleotides long; and the like).

8

By "nucleic acid molecule" as used herein is meant a molecule having nucleotides. The nucleic acid can be single, double or multiple stranded and may comprise modified or unmodified nucleotides or non-nucleotides or various mixtures and combinations thereof. An example of a nucleic acid molecule according to the

5   invention is a gene which encodes for macromolecule such as a protein.

In preferred embodiments of the present invention, a nucleic acid molecule, e.g., an antisense molecule, a triplex DNA, or an enzymatic nucleic acid molecule, is 13 to 100 nucleotides in length, e.g., in specific embodiments 35, 36, 37, or 38 nucleotides in length (e.g., for particular ribozymes). In particular embodiments, the

10   nucleic acid molecule is 15-100, 17-100, 20-100, 21-100, 23-100, 25-100, 27-100, 30-100, 32-100, 35-100, 40-100, 50-100, 60-100, 70-100, or 80-100 nucleotides in length. Instead of 100 nucleotides being the upper limit on the length ranges specified above, the upper limit of the length range can be, for example, 30, 40, 50, 60, 70, or 80 nucleotides. Thus, for any of the length ranges, the length range for

15   particular embodiments has lower limit as specified, with an upper limit as specified which is greater than the lower limit. For example, in a particular embodiment, the length range can be 35-50 nucleotides in length. All such ranges are expressly included. Also in particular embodiments, a nucleic acid molecule can have a length which is any of the lengths specified above, for example, 21 nucleotides in length.

20   By "complementarity" is meant that a nucleic acid can form hydrogen bond(s) with another RNA sequence by either traditional Watson-Crick or other non-traditional types. In reference to the nucleic molecules of the present invention, the binding free energy for a nucleic acid molecule with its target or complementary sequence is sufficient to allow the relevant function of the nucleic acid to proceed,

25   e.g., enzymatic nucleic acid cleavage, antisense or triple helix inhibition. Determination of binding free energies for nucleic acid molecules is well-known in the art (see, e.g., Turner *et al.*, 1987, CSH Symp. Quant. Biol. LII pp.123-133; Frier *et al.*, 1986, Proc. Nat. Acad. Sci. USA 83:9373-9377; Turner et al., 1987, J. Am. Chem. Soc. 109:3783-3785. A percent complementarity indicates the percentage of

30   contiguous residues in a nucleic acid molecule which can form hydrogen bonds (e.g., Watson-Crick base pairing) with a second nucleic acid sequence (e.g., 5, 6, 7, 8, 9, 10 out of 10 being 50%, 60%, 70%, 80%, 90%, and 100% complementary). "Perfectly complementary" means that all the contiguous residues of a nucleic acid sequence will hydrogen bond with the same number of contiguous residues in a

35   second nucleic acid sequence.

In yet another preferred embodiment, the modified nucleotide triphosphates of the instant invention can be used for combinatorial chemistry or *in vitro* selection of nucleic acid molecules with novel function. Modified oligonucleotides can be enzymatically synthesized to generate libraries for screening.

5   In another preferred embodiment, the invention features nucleic acid based techniques (e.g., enzymatic nucleic acid molecules), antisense nucleic acids, 2-5A antisense chimeras, triplex DNA, antisense nucleic acids containing RNA cleaving chemical groups) isolated using the methods described in this invention and methods for their use to diagnose, down regulate or inhibit gene expression.

10   By "inhibit" it is meant that the activity of target genes or level of mRNAs or equivalent RNAs encoding target genes is reduced below that observed in the absence of the nucleic acid molecules of the instant invention (e.g., enzymatic nucleic acid molecules), antisense nucleic acids, 2-5A antisense chimeras, triplex DNA, antisense nucleic acids containing RNA cleaving chemical groups). In one

15   embodiment, inhibition with enzymatic nucleic acid molecule preferably is below that level observed in the presence of an enzymatically attenuated nucleic acid molecule that is able to bind to the same site on the mRNA, but is unable to cleave that RNA. In another embodiment, inhibition with nucleic acid molecules, including enzymatic nucleic acid and antisense molecules, is preferably greater than that

20   observed in the presence of for example, an oligonucleotide with scrambled sequence or with mismatches. In another embodiment, inhibition of target genes with the nucleic acid molecule of the instant invention is greater than in the presence of the nucleic acid molecule than in its absence.

         In yet another preferred embodiment, the invention features a process for the
25   incorporating a plurality of compounds of formula I.

         In yet another embodiment, the invention features a nucleic acid molecule with catalytic activity having formula II:
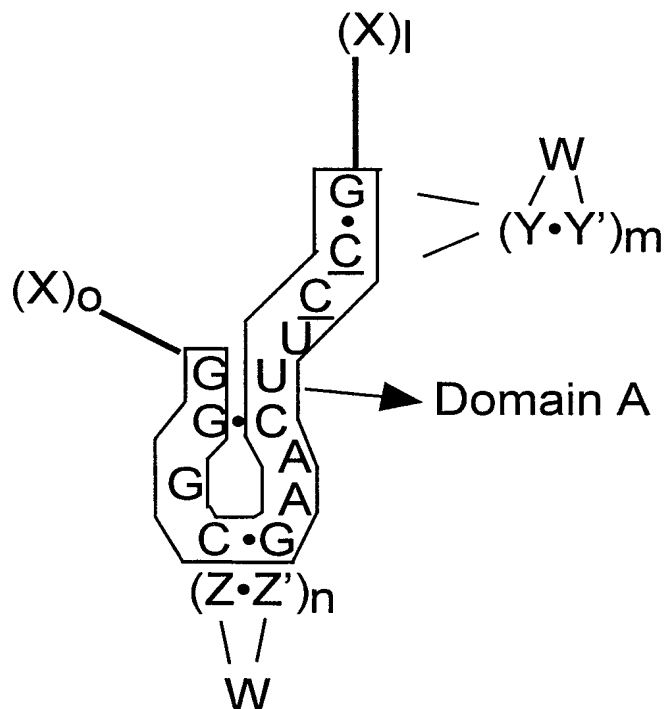
In the formula shown above X, Y, and Z represent independently a nucleotide or a non-nucleotide linker, which may be same or different; • indicates hydrogen bond formation between two adjacent nucleotides; Y' is a nucleotide complementary

5   to Y; Z' is a nucleotide complementary to Z; l is an integer greater than or equal to 3 and preferably less than 20, more specifically 4, 5, 6, 7, 8, 9, 10, 11, 12, or 15; m is an integer greater than 1 and preferably less than 10, more specifically 2, 3, 4, 5, 6, or 7; n is an integer greater than 1 and preferably less than 10, more specifically 3, 4, 5, 6, or 7; o is an integer greater than or equal to 3 and preferably less than 20, more

10   specifically 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, or 15; l and o may be the same length (l = o) or different lengths (l ≠ o); each X(l) and X(o) are oligonucleotides which are of sufficient length to stably interact independently with a target nucleic acid sequence (the target can be an RNA, DNA or RNA/DNA mixed polymers); W is a linker or ≥ 2 nucleotides in length or may be a non-nucleotide linker; A, U, C, and G represent

15   the nucleotides; G is a nucleotide, preferably 2'-O-methyl; $\underline{C}$ represents a nucleotide, preferably 2'-amino (e.g., 2'-NH_2 or 2'-O- NH_2, and _____ represents a chemical linkage (*e.g.* a phosphate ester linkage, amide linkage, phosphorothioate, phosphorodithioate or others known in the art).

The enzymatic nucleic acid molecule of Formula II may independently comprise a cap structure which may independently be present or absent.

By "sufficient length" is meant an oligonucleotide of greater than or equal to 3 nucleotides.

5   By "stably interact" is meant, interaction of the oligonucleotides with target nucleic acid (*e.g.*, by forming hydrogen bonds with complementary nucleotides in the target under physiological conditions).

By "chimeric nucleic acid molecule" or "chimeric oligonucleotide" is meant that, the molecule may be comprised of both modified or unmodified DNA or RNA.

10   By "cap structure" is meant chemical modifications, which have been incorporated at the terminus of the oligonucleotide. These terminal modifications protect the nucleic acid molecule from exonuclease degradation, and may help in delivery and/or localization within a cell. The cap may be present at the 5'-terminus (5'-cap) or at the 3'-terminus (3'-cap) or may be present on both terminus. In non-limiting examples: the 5'-cap is selected from the group comprising inverted abasic residue (moiety), 4',5'-methylene nucleotide; 1-(beta-D-erythrofuranosyl) nucleotide, 4'-thio nucleotide, carbocyclic nucleotide; 1,5-anhydrohexitol nucleotide; L-nucleotides; alpha-nucleotides; modified base nucleotide; phosphorodithioate linkage; *threo*-pentofuranosyl nucleotide; acyclic 3',4'-seco nucleotide; acyclic 3,4-dihydroxybutyl nucleotide; acyclic 3,5-dihydroxypentyl nucleotide, 3'-3'-inverted nucleotide moiety; 3'-3'-inverted abasic moiety; 3'-2'-inverted nucleotide moiety; 3'-2'-inverted abasic moiety; 1,4-butanediol phosphate; 3'-phosphoramidate; hexylphosphate; aminohexyl phosphate; 3'-phosphate; 3'-phosphorothioate; phosphorodithioate; or bridging or non-bridging methylphosphonate moiety (for more details see Beigelman *et al.*, International PCT publication No. WO 97/26270, incorporated by reference herein). In yet another preferred embodiment the 3'-cap is selected from a group comprising, 4',5'-methylene nucleotide; 1-(beta-D-erythrofuranosyl) nucleotide; 4'-thio nucleotide, carbocyclic nucleotide; 5'-amino-alkyl phosphate; 1,3-diamino-2-propyl phosphate, 3-aminopropyl phosphate; 6-aminohexyl phosphate; 1,2-aminododecyl phosphate; hydroxypropyl phosphate; 1,5-anhydrohexitol nucleotide; L-nucleotide; alpha-nucleotide; modified base nucleotide; phosphorodithioate; *threo*-pentofuranosyl nucleotide; acyclic 3',4'-seco nucleotide; 3,4-dihydroxybutyl nucleotide; 3,5-dihydroxypentyl nucleotide, 5'-5'-inverted nucleotide moeity; 5'-5'-inverted abasic moeity; 5'-phosphoramidate; 5'-

phosphorothioate; 1,4-butanediol phosphate; 5'-amino; bridging and/or non-bridging 5'-phosphoramidate, phosphorothioate and/or phosphorodithioate, bridging or non bridging methylphosphonate and 5'-mercapto moeities (for more details see Beaucage and Iyer, 1993, *Tetrahedron* 49, 1925; incorporated by reference herein). By the term "non-nucleotide" is meant any group or compound which can be incorporated into a nucleic acid chain in the place of one or more nucleotide units, including either sugar and/or phosphate substitutions, and allows the remaining bases to exhibit their enzymatic activity. The group or compound is abasic in that it does not contain a commonly recognized nucleotide base, such as adenosine, guanine, cytosine, uracil or thymine. The terms "abasic" or "abasic nucleotide" as used herein encompass sugar moieties lacking a base or having other chemical groups in place of base at the 1' position.

In connection with 2'-modified nucleotides as described for the present invention, by "amino" is meant $2'$-NH_2 or $2'$-O-NH_2, which may be modified or un-modified. Such modified groups are described, for example, in Eckstein et al., U.S. Patent 5,672,695 and Matulic-Adamic et al., WO 98/28317, respectively, which are both incorporated by reference in their entireties.

Description of the Preferred Embodiments

The drawings will first briefly be described.

Drawings:

Figure 1 displays a schematic representation of NTP synthesis using nucleoside substrates.

Figure 2 shows a scheme for an *in vitro* selection method. A pool of nucleic acid molecules is generated with a random core region and one or more region(s) with a defined sequence. These nucleic acid molecules are bound to a column containing immobilized oligonucleotide with a defined sequence, where the defined sequence is complementary to region(s) of defined sequence of nucleic acid molecules in the pool. Those nucleic acid molecules capable of cleaving the immobilized oligonucleotide (target) in the column are isolated and converted to complementary DNA (cDNA), followed by transcription using NTPs to form a new nucleic acid pool.

Figure 3 shows a scheme for a two column *in vitro* selection method. A pool of nucleic acid molecules is generated with a random core and two flanking regions (region A and region B) with defined sequences. The pool is passed through a column which has immobilized oligonucleotides with regions A' and B' that are complementary to regions A and B of the nucleic acid molecules in the pool, respectively. The column is subjected to conditions sufficient to facilitate cleavage of the immobilized oligonucleotide target. The molecules in the pool that cleave the target (active molecules) have A' region of the target bound to their A region, whereas the B region is free. The column is washed to isolate the active molecules with the bound A' region of the target. This pool may of active molecules may also contain some molecules that are not active to cleave the target (inactive molecules) but have dissociated from the column. To separate the contaminating inactive molecules from the active molecules, the pool is passed through a second column (column 2) which contains immobilized oligonucleotides with the A' sequence but not the B' sequence. The inactive molecules will bind to column 2 but the active molecules will not bind to column 2 because their A region is occupied by the A' region of the target oligonucleotide from column 1. The column 2 is washed to isolate the active molecules for further processing as described under figure 2 scheme.

Figure 4 is a diagram of a novel 48 nucleotide enzymatic nucleic acid motif which was identified using *in vitro* methods described in the instant invention. The molecule shown is only exemplary. The 5' and 3' terminal nucleotides (referring to the nucleotides of the substrate binding arms rather than merely the single terminal nucleotide on the 5' and 3' ends) can be varied so long as those portions can base-pair with target substrate sequence. In addition, the guanosine (G) shown at the cleavage site of the substrate can be changed to other nucleotides so long as the change does not eliminate the ability of enzymatic nucleic acid molecules to cleave the target sequence. Substitutions in the nucleic acid molecule and/or in the substrate sequence can be readily tested, for example, as described herein.

Figure 5 is a schematic diagram of HCV luciferase assay used to demonstrate efficacy of class I enzymatic nucleic acid molecule motif.

Figure 6 is a graph indicating the dose curve of an enzymatic nucleic acid molecule targeting site 146 on HCV RNA.

14

Figure 7 is a bar graph showing enzymatic nucleic acid molecules targeting 4 sites within the HCV RNA are able to reduce RNA levels in cells.

Figure 8 shows secondary structures and cleavage rates for characterized Class II enzymatic nucleic acid motifs.

Nucleotide Synthesis

Addition of dimethylaminopyridine (DMAP) to the phosphorylation protocols known in the art can greatly increase the yield of nucleotide monophosphates while decreasing the reaction time (Fig. 1). Synthesis of the nucleosides of the invention have been described in several publications and Applicants previous applications (Beigelman et al., International PCT publication No. WO 96/18736; Dudzcy et al., Int. PCT Pub. No. WO 95/11910; Usman et al., Int. PCT Pub. No. WO 95/13378; Matulic-Adamic et al., 1997, Tetrahedron Lett. 38, 203; Matulic-Adamic et al., 1997, Tetrahedron Lett. 38, 1669; all of which are incorporated herein by reference). These nucleosides are dissolved in triethyl phosphate and chilled in an ice bath. Phosphorus oxychloride ($POCl_3$) is then added followed by the introduction of DMAP. The reaction is then warmed to room temperature and allowed to proceed for 5 hours. This reaction allows the formation of nucleotide monophosphates which can then be used in the formation of nucleotide triphosphates. Tributylamine is added followed by the addition of anhydrous acetonitrile and tributylammonium pyrophosphate. The reaction is then quenched with TEAB and stirred overnight at room temperature (about 20°C). The triphosphate is purified using column purification and HPLC and the chemical structure is confirmed using NMR analysis. Those skilled in the art will recognize that the reagents, temperatures of the reaction, and purification methods can easily be alternated with substitutes and equivalents and still obtain the desired product.

Nucleotide Triphosphates

The invention provides nucleotide triphosphates which can be used for a number of different functions. The nucleotide triphosphates formed from nucleosides found in table I are unique and distinct from other nucleotide triphosphates known in the art. Incorporation of modified nucleotides into DNA or RNA oligonucleotides can alter the properties of the molecule. For example, modified nucleotides can hinder binding of nucleases, thus increasing the chemical

half-life of the molecule. This is especially important if the molecule is to be used for cell culture or *in vivo*. It is known in the art that the introduction of modified nucleotides into these molecules can greatly increase the stability and thereby the effectiveness of the molecules (Burgin *et al.*, 1996, *Biochemistry* 35, 14090-14097; Usman *et al.*, 1996, *Curr. Opin. Struct. Biol.* 6, 527-533).

Modified nucleotides are incorporated using either wild type and mutant polymerases. For example, mutant T7 polymerase is used in the presence of modified nucleotide triphosphate(s), DNA template and suitable buffers. Those skilled in the art will recognize that other polymerases and their respective mutant versions can also be utilized for the incorporation of NTP's of the invention. Nucleic acid transcripts were detected by incorporating radiolabelled nucleotides (α-^{32}P NTP). The radiolabeled NTP contained the same base as the modified triphosphate being tested. The effects of methanol, PEG and LiCl were tested by adding these compounds independently or in combination. Detection and quantitation of the nucleic acid transcripts was performed using a Molecular Dynamics PhosphorImager. Efficiency of transcription was assessed by comparing modified nucleotide triphosphate incorporation with all-ribonucleotide incorporation control. Wild type polymerase was used to incorporate NTP's using the manufacturer's buffers and instructions (Boehringer Mannheim).

Transcription Conditions

Incorporation rates of modified nucleotide triphosphates into oligonucleotides can be increased by adding to traditional buffer conditions, several different enhancers of modified NTP incorporation. Applicant has utilized methanol and LiCl in an attempt to increase incorporation rates of dNTP using RNA polymerase. These enhancers of modified NTP incorporation can be used in different combinations and ratios to optimize transcription. Optimal reaction conditions differ between nucleotide triphosphates and can readily be determined by standard experimentation. Overall however, inclusion of enhancers of modified NTP incorporation such as methanol or inorganic compound such as lithium chloride, have been shown by the applicant to increase the mean transcription rates.

Mechanism of action of Nucleic Acid Molecules of the Invention

Antisense: Antisense molecules may be modified or unmodified RNA, DNA, or mixed polymer oligonucleotides and primarily function by specifically binding to matching sequences resulting in inhibition of peptide synthesis (Wu-Pong, Nov

1994, *BioPharm*, 20-33). The antisense oligonucleotide binds to target RNA by Watson Crick base-pairing and blocks gene expression by preventing ribosomal translation of the bound sequences either by steric blocking or by activating RNase H enzyme. Antisense molecules may also alter protein synthesis by interfering with RNA processing or transport from the nucleus into the cytoplasm (Mukhopadhyay & Roth, 1996, *Crit. Rev. in Oncogenesis* 7, 151-190).

In addition, binding of single stranded DNA to RNA may result in nuclease degradation of the heteroduplex (Wu-Pong, *supra*; Crooke, *supra*). To date, the only backbone modified DNA chemistry which will act as substrates for RNase H are phosphorothioates and phosphorodithioates. Recently it has been reported that 2'-arabino and 2'-fluoro arabino- containing oligos can also activate RNase H activity.

A number of antisense molecules have been described that utilize novel configurations of chemically modified nucleotides, secondary structure, and/or RNase H substrate domains (Woolf *et al.*, International PCT Publication No. WO 98/13526; Thompson *et al.*, USSN 60/082,404 which was filed on April 20, 1998; Hartmann *et al.*, USSN 60/101,174 which was filed on September 21, 1998) all of these are incorporated by reference herein in their entirety.

Triplex Forming Oligonucleotides (TFO): Single stranded DNA may be designed to bind to genomic DNA in a sequence specific manner. TFOs are comprised of pyrimidine-rich oligonucleotides which bind DNA helices through Hoogsteen Base-pairing (Wu-Pong, *supra*)The resulting triple helix composed of the DNA sense, DNA antisense, and TFO disrupts RNA synthesis by RNA polymerase. The TFO mechanism may result in gene expression or cell death since binding may be irreversible (Mukhopadhyay & Roth, *supra*)

2-5A Antisense Chimera: The 2-5A system is an interferon-mediated mechanism for RNA degradation found in higher vertebrates (Mitra *et al.*, 1996, *Proc Nat Acad Sci USA* 93, 6780-6785). Two types of enzymes, 2-5A synthetase and RNase L, are required for RNA cleavage. The 2-5A synthetases require double stranded RNA to form 2'-5' oligoadenylates (2-5A). 2-5A then acts as an allosteric effector for utilizing RNase L which has the ability to cleave single stranded RNA. The ability to form 2-5A structures with double stranded RNA makes this system particularly useful for inhibition of viral replication.

(2'-5') oligoadenylate structures may be covalently linked to antisense molecules to form chimeric oligonucleotides capable of RNA cleavage (Torrence,

supra). These molecules putatively bind and activate a 2-5A dependent RNase, the oligonucleotide/enzyme complex then binds to a target RNA molecule which can then be cleaved by the RNase enzyme.

Enzymatic Nucleic Acid: In general, enzymatic nucleic acids act by first
5   binding to a target RNA. Such binding occurs through the target binding portion of an enzymatic nucleic acid which is held in close proximity to an enzymatic portion of the molecule that acts to cleave the target RNA. Thus, the enzymatic nucleic acid first recognizes and then binds a target RNA through complementary base-pairing, and once bound to the correct site, acts enzymatically to cut the target RNA.
10   Strategic cleavage of such a target RNA will destroy its ability to direct synthesis of an encoded protein. After an enzymatic nucleic acid has bound and cleaved its RNA target, it is released from that RNA to search for another target and can repeatedly bind and cleave new targets.

The enzymatic nature of an enzymatic nucleic acid has significant advantages,
15   such as the concentration of enzymatic nucleic acid molecules necessary to affect a therapeutic treatment is lower. This advantage reflects the ability of the enzymatic nucleic acid molecules to act enzymatically. Thus, a single enzymatic nucleic acid molecule is able to cleave many molecules of target RNA. In addition, the enzymatic nucleic acid molecule is a highly specific inhibitor, with the specificity of
20   inhibition depending not only on the base-pairing mechanism of binding to the target RNA, but also on the mechanism of target RNA cleavage. Single mismatches, or base-substitutions, near the site of cleavage can be chosen to completely eliminate catalytic activity of enzymatic nucleic acid molecules.

Nucleic acid molecules having an endonuclease enzymatic activity are able to
25   repeatedly cleave other separate RNA molecules in a nucleotide base sequence-specific manner. Such enzymatic nucleic acid molecules can be targeted to virtually any RNA transcript, and efficient cleavage achieved *in vitro* (Zaug *et al.*, 324, *Nature* 429 1986 ; Uhlenbeck, 1987 *Nature* 328, 596; Kim et al., 84 *Proc. Natl. Acad. Sci. USA* 8788, 1987; Dreyfus, 1988, *Einstein Quart. J. Bio. Med.*, 6, 92;
30   Haseloff and Gerlach, 334 *Nature* 585, 1988; Cech, 260 *JAMA* 3030, 1988; and Jefferies et al., 17 *Nucleic Acids Research* 1371, 1989; Santoro *et al.*, 1997 *supra*).

Because of their sequence-specificity, *trans*-cleaving enzymatic nucleic acid molecules show promise as therapeutic agents for human disease (Usman & McSwiggen, 1995 *Ann. Rep. Med. Chem.* **30**, 285-294; Christoffersen and Marr,

1995 *J. Med. Chem.* **38**, 2023-2037). Enzymatic nucleic acid molecules can be designed to cleave specific RNA targets within the background of cellular RNA. Such a cleavage event renders the RNA non-functional and abrogates protein expression from that RNA. In this manner, synthesis of a protein associated with a disease state can be selectively inhibited.

Optimizing Nucleic Acid Catalyst Activity

Catalytic activity of the enzymatic nucleic acid molecules described and identified using the methods of the instant invention, can be optimized as described by Draper et al., *supra* and using the methods well known in the art. The details will not be repeated here, but include altering the length of the enzymatic nucleic acid molecules' binding arms, or chemically synthesizing enzymatic nucleic acid molecules with modifications (base, sugar and/or phosphate) that prevent their degradation by serum ribonucleases and/or enhance their enzymatic activity (see *e.g.,* Eckstein *et al.,* International Publication No. WO 92/07065; Perrault *et al.,* 1990 *Nature* 344, 565; Pieken et al., 1991 *Science* 253, 314; Usman and Cedergren, 1992 *Trends in Biochem. Sci.* 17, 334; Usman *et al.,* International Publication No. WO 93/15187; Rossi *et al.,* International Publication No. WO 91/03162; Sproat, US Patent No. 5,334,711; and Burgin *et al., supra;* all of these describe various chemical modifications that can be made to the base, phosphate and/or sugar moieties of enzymatic nucleic acid molecules). Modifications which enhance their efficacy in cells, and removal of bases from stem loop structures to shorten synthesis times and reduce chemical requirements are desired. (All these publications are hereby incorporated by reference herein).

There are several examples in the art describing sugar, base and phosphate modifications that can be introduced into nucleic acid molecules (e.g., enzymatic nucleic acid molecules) without significantly effecting catalysis and with significant enhancement in their nuclease stability and efficacy. Enzymatic nucleic acid molecules are modified to enhance stability and/or enhance catalytic activity by modification with nuclease resistant groups, for example, 2'-amino, 2'-*C*-allyl, 2'-fluoro, 2'-*O*-methyl, 2'-H, nucleotide base modifications (for a review see Usman and Cedergren, 1992 *TIBS* 17, 34; Usman *et al.,* 1994 *Nucleic Acids Symp. Ser.* 31, 163; Burgin *et al.,* 1996 *Biochemistry* 35, 14090). Sugar modification of enzymatic nucleic acid molecules have been extensively described in the art (see Eckstein *et al., International Publication* PCT No. WO 92/07065; Perrault *et al. Nature* 1990, *344,* 565-568; Pieken *et al. Science* 1991, *253,* 314-317; Usman and Cedergren,

Trends in Biochem. Sci. 1992, *17*, 334-339; Usman *et al.* *International Publication* PCT No. WO 93/15187; Sproat, *US Patent* No. 5,334,711 and Beigelman *et al.,* 1995 *J. Biol. Chem.* 270, 25702; all of the references are hereby incorporated in their totality by reference herein). Such publications describe general methods and strategies to determine the location of incorporation of sugar, base and/or phosphate modifications and the like into s without inhibiting catalysis, and are incorporated by reference herein. In view of such teachings, similar modifications can be used as described herein to modify the nucleic acid catalysts of the instant invention.

Nucleic acid catalysts having chemical modifications which maintain or enhance enzymatic activity are provided. Such nucleic acid molecules are generally more resistant to nucleases than unmodified nucleic acid. Thus, in a cell and/or *in vivo* the activity may not be significantly lowered. As exemplified herein such enzymatic nucleic acid molecules are useful in a cell and/or *in vivo* even if activity over all is reduced 10 fold (Burgin *et al.,* 1996, *Biochemistry*, 35, 14090). Such enzymatic nucleic acid molecules herein are said to "maintain" the enzymatic activity.

Therapeutic nucleic acid molecules (e.g., enzymatic nucleic acid molecules and antisense nucleic acid molecules) delivered exogenously must optimally be stable within cells until translation of the target RNA has been inhibited long enough to reduce the levels of the undesirable protein. This period of time varies between hours to days depending upon the disease state. Clearly, these nucleic acid molecules must be resistant to nucleases in order to function as effective intracellular therapeutic agents. Improvements in the chemical synthesis of nucleic acid molecules described in the instant invention and in the art have expanded the ability to modify nucleic acid molecules by introducing nucleotide modifications to enhance their nuclease stability as described above.

By "enhanced enzymatic activity" is meant to include activity measured in cells and/or *in vivo* where the activity is a reflection of both catalytic activity and enzymatic nucleic acid molecules stability. In this invention, the product of these properties is increased or not significantly (less that 10 fold) decreased *in vivo* compared to an unmodified enzymatic nucleic acid molecules.

In yet another preferred embodiment, nucleic acid catalysts having chemical modifications which maintain or enhance enzymatic activity is provided. Such nucleic acid is also generally more resistant to nucleases than unmodified nucleic

20

acid. Thus, in a cell and/or *in vivo* the activity may not be significantly lowered. As exemplified herein such enzymatic nucleic acid molecules are useful in a cell and/or *in vivo* even if activity over all is reduced 10 fold (Burgin *et al.,* 1996, *Biochemistry*, 35, 14090). Such enzymatic nucleic acid molecules herein are said to "maintain" the enzymatic activity on all RNA enzymatic nucleic acid molecule.

Use of these molecules will lead to better treatment of the disease progression by affording the possibility of combination therapies (e.g., multiple enzymatic nucleic acid molecules targeted to different genes, enzymatic nucleic acid molecules coupled with known small molecule inhibitors, or intermittent treatment with combinations of enzymatic nucleic acid molecules (including different enzymatic nucleic acid molecules motifs) and/or other chemical or biological molecules). The treatment of patients with nucleic acid molecules may also include combinations of different types of nucleic acid molecules. Therapies may be devised which include a mixture of enzymatic nucleic acid molecules (including different enzymatic nucleic acid molecules motifs), antisense and/or 2-5A chimera molecules to one or more targets to alleviate symptoms of a disease.

Administration of nucleotide mono, di or triphosphates and Nucleic Acid Molecules

The nucleotide monophosphates, diphosphates, or triphosphates or the nucleic acid molecules of the instant invention, can be used as a therapeutic agent either independently or in combination with other pharmaceutical components. These molecules of the inventions can be administered to patients using the methods of Sullivan *et al.,* PCT WO 94/02595 Akhtar *et al.,* 1992, *Trends Cell Bio.,* 2, 139; and *Delivery Strategies for Antisense Oligonucleotide Therapeutics,* ed. Akhtar, 1995 which are both incorporated herein by reference. Molecules of the invention may be administered to cells by a variety of methods known to those familiar to the art, including, but not restricted to, encapsulation in liposomes, by iontophoresis, or by incorporation into other vehicles, such as hydrogels, cyclodextrins, biodegradable nanocapsules, and bioadhesive microspheres. For some indications, enzymatic nucleic acid molecules may be directly delivered *ex vivo* to cells or tissues with or without the aforementioned vehicles. Alternatively, the modified nucleotide triphosphate, diphosphate or monophosphate/vehicle combination is locally delivered by direct injection or by use of a catheter, infusion pump or stent. Other routes of delivery include, but are not limited to, intravascular, intramuscular, subcutaneous or joint injection, aerosol inhalation, oral (tablet or pill form), topical, systemic, ocular, intraperitoneal and/or intrathecal delivery. More detailed

descriptions of delivery and administration are provided in Sullivan *et al.*, supra and Draper *et al.*, PCT WO93/23569 which have been incorporated by reference herein.

The molecules of the instant invention can be used as pharmaceutical agents. Pharmaceutical agents prevent, inhibit the occurrence, or treat (alleviate a symptom to some extent, preferably all of the symptoms) of a disease state in a patient.

The negatively charged nucleotide mono, di or triphosphates of the invention can be administered and introduced into a patient by any standard means, with or without stabilizers, buffers, and the like, to form a pharmaceutical composition. When it is desired to use a liposome delivery mechanism, standard protocols for formation of liposomes can be followed. The compositions of the present invention may also be formulated and used as tablets, capsules or elixirs for oral administration; suppositories for rectal administration; sterile solutions; suspensions for injectable administration; and the like.

The present invention also includes pharmaceutically acceptable formulations of the compounds described. These formulations include salts of the above compounds, *e.g.*, ammonium, sodium, calcium, magnesium, lithium, and potassium salts.

A pharmacological composition or formulation refers to a composition or formulation in a form suitable for administration, *e.g.*, systemic administration, into a cell or patient, preferably a human. Suitable forms, in part, depend upon the use or the route of entry, for example oral, transdermal, or by injection. Such forms should not prevent the composition or formulation to reach a target cell (*i.e.*, a cell to which the negatively charged polymer is desired to be delivered to). For example, pharmacological compositions injected into the blood stream should be soluble. Other factors are known in the art, and include considerations such as toxicity and forms which prevent the composition or formulation from exerting its effect.

By "systemic administration" is meant *in* vivo systemic absorption or accumulation of drugs in the blood stream followed by distribution throughout the entire body. Administration routes which lead to systemic absorption include, without limitations: intravenous, subcutaneous, intraperitoneal, inhalation, oral, intrapulmonary and intramuscular. Each of these administration routes expose the desired negatively charged polymers, *e.g.*, NTP's, to an accessible diseased tissue. The rate of entry of a drug into the circulation has been shown to be a function of molecular weight or size. The use of a liposome or other drug carrier comprising the

compounds of the instant invention can potentially localize the drug, for example, in certain tissue types, such as the tissues of the reticular endothelial system (RES). A liposome formulation which can facilitate the association of drug with the surface of cells, such as, lymphocytes and macrophages is also useful. This approach may

5   provide enhanced delivery of the drug to target cells by taking advantage of the specificity of macrophage and lymphocyte immune recognition of abnormal cells, such as the cancer cells.

The invention also features the use of the a composition comprising surface-modified liposomes containing poly (ethylene glycol) lipids (PEG-modified, or

10   long-circulating liposomes or stealth liposomes). These formulations offer a method for increasing the accumulation of drugs in target tissues. This class of drug carriers resists opsonization and elimination by the mononuclear phagocytic system (MPS or RES), thereby enabling longer blood circulation times and enhanced tissue exposure for the encapsulated drug (Lasic *et al. Chem. Rev.* 1995, 95, 2601-2627; Ishiwata *et*

15   *al., Chem. Pharm. Bull.* 1995, 43, 1005-1011). Such liposomes have been shown to accumulate selectively in tumors, presumably by extravasation and capture in the neovascularized target tissues (Lasic *et al., Science* 1995, 267, 1275-1276; Oku *et al.,* 1995, *Biochim. Biophys. Acta,* 1238, 86-90). The long-circulating liposomes enhance the pharmacokinetics and pharmacodynamics of drugs, particularly

20   compared to conventional cationic liposomes which are known to accumulate in tissues of the MPS (Liu *et al., J. Biol. Chem.* 1995, 42, 24864-24870; Choi *et al.,* International PCT Publication No. WO 96/10391; Ansell *et al.,* International PCT Publication No. WO 96/10390; Holland *et al.,* International PCT Publication No. WO 96/10392; all of these are incorporated by reference herein). Long-circulating

25   liposomes are also likely to protect drugs from nuclease degradation to a greater extent compared to cationic liposomes, based on their ability to avoid accumulation in metabolically aggressive MPS tissues such as the liver and spleen. All of these references are incorporated by reference herein.

The present invention also includes compositions prepared for storage or

30   administration which include a pharmaceutically effective amount of the desired compounds in a pharmaceutically acceptable carrier or diluent. Acceptable carriers or diluents for therapeutic use are well known in the pharmaceutical art, and are described, for example, in *Remington's Pharmaceutical Sciences*, Mack Publishing Co. (A.R. Gennaro edit. 1985) hereby incorporated by reference herein. For

35   example, preservatives, stabilizers, dyes and flavoring agents may be provided. *Id.*

at 1449. These include sodium benzoate, sorbic acid and esters of *p*-hydroxybenzoic acid. In addition, antioxidants and suspending agents may be used.

By "patient" is meant an organism which is a donor or recipient of explanted cells or the cells themselves. "Patient" also refers to an organism to which the compounds of the invention can be administered. Preferably, a patient is a mammal, *e.g.*, a human, primate or a rodent.

A pharmaceutically effective dose is that dose required to prevent, inhibit the occurrence, or treat (alleviate a symptom to some extent, preferably all of the symptoms) of a disease state. The pharmaceutically effective dose depends on the type of disease, the composition used, the route of administration, the type of mammal being treated, the physical characteristics of the specific mammal under consideration, concurrent medication, and other factors which those skilled in the medical arts will recognize. Generally, an amount between 0.1 mg/kg and 100 mg/kg body weight/day of active ingredients is administered dependent upon potency of the negatively charged polymer. In a one aspect, the invention provides enzymatic nucleic acid molecules that can be delivered exogenously to specific cells as required.

The nucleic acid molecules of the present invention may also be administered to a patient in combination with other therapeutic compounds to increase the overall therapeutic effect. The use of multiple compounds to treat an indication may increase the beneficial effects while reducing the presence of side effects.

Examples

The following are non-limiting examples showing the synthesis, incorporation and analysis of nucleotide triphosphates and activity of enzymatic nucleic acids of the instant invention.

Applicant synthesized pyrimidine nucleotide triphosphates using DMAP in the reaction. For purines, applicant utilized standard protocols previously described in the art (Yoshikawa *et al supra;*. Ludwig, supra). Described below is one example of a pyrimdine nucleotide triphosphate and one purine nucleotide triphosphate synthesis.

24

Example 1: Synthesis of purine nucleotide triphosphates: 2'-*O*-methyl-guanosine-5'-triphosphate

      2'-*O*-methyl guanosine nucleoside (0.25 grams, 0.84 mmol) was dissolved in triethyl phosphate (5.0) ml by heating to 100°C for 5 minutes. The resulting clear,

5   colorless solution was cooled to 0°C using an ice bath under an argon atmosphere. Phosphorous oxychloride (1.8 eq., 0.141 ml) was then added to the reaction mixture with vigorous stirring. The reaction was monitored by HPLC, using a sodium perchlorate gradient. After 5 hours at 0°C, tributylamine (0.65 ml) was added followed by the addition of anhydrous acetonitrile (10.0 ml), and after 5 minutes

10   (reequilibration to 0°C) tributylammonium pyrophosphate (4.0 eq., 1.53 g) was added. The reaction mixture was quenched with 20 ml of 2M TEAB after 15 minutes at 0°C (HPLC analysis with above conditions showed consumption of monophosphate at 10 minutes) then stirred overnight at room temperature, the mixture was evaporated *in vacuo* with methanol co-evaporation (4x) then diluted in

15   50 ml 0.05M TEAB. DEAE sephadex purification was used with a gradient of 0.05 to 0.6 M TEAB to obtain pure triphosphate (0.52 g, 66.0% yield) (elutes around 0.3M TEAB); the purity was confirmed by HPLC and NMR analysis.

Example 2: Synthesis of Pyrimdine nucleotide triphosphates: 2'-*O*-methylthiomethyl-uridine-5'-triphosphate

20   2'-*O*-methylthiomethyl uridine nucleoside (0.27 grams, 1.0 mmol) was dissolved in triethyl phosphate (5.0 ml). The resulting clear, colorless solution was cooled to 0°C with an ice bath under an argon atmosphere. Phosphorus oxychloride (2.0 eq., 0.190 ml) was then added to the reaction mixture with vigorous stirring. Dimethylaminopyridine (DMAP, 0.2eq., 25 mg) was added, the solution warmed to

25   room temperature and the reaction was monitored by HPLC, using a sodium perchlorate gradient. After 5 hours at 20°C, tributylamine (1.0 ml) was added followed by anhydrous acetonitrile (10.0 ml), and after 5 minutes tributylammonium pyrophosphate (4.0 eq., 1.8 g) was added. The reaction mixture was quenched with 20 ml of 2M TEAB after 15 minutes at 20°C (HPLC analysis with above conditions

30   showed consumption of monophosphate at 10 minutes) then stirred overnight at room temperature. The mixture was evaporated *in vacuo* with methanol co-evaporation (4x) then diluted in 50 ml 0.05M TEAB. DEAE fast flow Sepharose purification with a gradient of 0.05 to 1.0 M TEAB was used to obtain pure triphosphate (0.40 g, 44% yield) (elutes around 0.3M TEAB) as determined by

35   HPLC and NMR analysis.

Example 3: Utilization of DMAP in Uridine 5'-Triphosphate Synthesis

The reactions were performed on 20 mg aliquots of nucleoside dissolved in 1 ml of triethyl phosphate and 19 ul of phosphorus oxychloride. The reactions were monitored at 40 minute intervals automatically by HPLC to generate yield-of-product curves at times up to 18 hours. A reverse phase column and ammonium acetate/ sodium acetate buffer system (50mM & 100mM respectively at pH 4.2) was used to separate the 5', 3', 2' monophosphates (the monophosphates elute in that order) from the 5'-triphosphate and the starting nucleoside. The data is shown in table 2. These conditions doubled the product yield and resulted in a 10-fold improvement in the reaction time to maximum yield (1200 minutes down to 120 minutes for a 90% yield). Selectivity for 5'-monophosphorylation was observed for all reactions. Subsequent triphosphorylation occurred in nearly quantitative yield.

Materials Used in Bacteriophage T7 RNA Polymerase Reactions

Buffer 1: Reagents are mixed together to form a 10X stock solution of buffer 1 (400 mM Tris-Cl (pH 8.1), 200 mM $MgCl_2$, 100 mM DTT, 50 mM spermidine, and 0.1% triton X-100. Prior to initiation of the polymerase reaction methanol, LiCl is added and the buffer is diluted such that the final reaction conditions for condition 1 consisted of : 40mM tris pH (8.1), 20mM $MgCl_2$, 10 mM DTT, 5 mM spermidine, 0.01% triton X-100, 10% methanol, and 1 mM LiCl.

BUFFER 2: Reagents are mixed together to form a 10X stock solution of buffer 2(400 mM Tris-Cl (pH 8.1), 200 mM $MgCl_2$, 100 mM DTT, 50 mM spermidine, and 0.1% triton X-100. Prior to initiation of the polymerase reaction PEG, LiCl is added and the buffer is diluted such that the final reaction conditions for buffer 2 consisted of : 40mM tris pH (8.1), 20mM $MgCl_2$, 10 mM DTT, 5 mM spermidine, 0.01% triton X-100, 4% PEG, and 1 mM LiCl.

BUFFER 3: Reagents are mixed together to form a 10X stock solution of buffer 3 (400 mM Tris-Cl (pH 8.0), 120 mM $MgCl_2$, 50 mM DTT, 10 mM spermidine and 0.02% triton X-100. Prior to initiation of the polymerase reaction PEG is added and the buffer is diluted such that the final reaction conditions for buffer 3 consisted of : 40mM tris pH (8.0), 12 mM $MgCl_2$, 5 mM DTT, 1 mM spermidine, 0.002% triton X-100, and 4% PEG.

BUFFER 4: Reagents are mixed together to form a 10X stock solution of buffer 4 (400 mM Tris-Cl (pH 8.0), 120 mM $MgCl_2$, 50 mM DTT, 10 mM spermidine and

0.02% triton X-100. Prior to initiation of the polymerase reaction PEG, methanol is added and the buffer is diluted such that the final reaction conditions for buffer 4 consisted of : 40mM tris pH (8.0), 12 mM $MgCl_2$, 5 mM DTT, 1 mM spermidine, 0.002% triton X-100, 10% methanol, and 4% PEG.

5   **BUFFER 5:** Reagents are mixed together to form a 10X stock solution of buffer 5 (400 mM Tris-Cl (pH 8.0), 120 mM $MgCl_2$, 50 mM DTT, 10 mM spermidine and 0.02% triton X-100. Prior to initiation of the polymerase reaction(PEG, LiCl is added and the buffer is diluted such that the final reaction conditions for buffer 5 consisted of : 40mM tris pH (8.0), 12 mM $MgCl_2$, 5 mM DTT, 1 mM spermidine,

10   0.002% triton X-100, 1 mM LiCl and 4% PEG.

BUFFER 6: Reagents are mixed together to form a 10X stock solution of buffer 6 (400 mM Tris-Cl (pH 8.0), 120 mM $MgCl_2$, 50 mM DTT, 10 mM spermidine and 0.02% triton X-100. Prior to initiation of the polymerase reaction PEG, methanol is added and the buffer is diluted such that the final reaction conditions for buffer 6

15   consisted of : 40mM tris pH (8.0), 12 mM $MgCl_2$, 5 mM DTT, 1 mM spermidine, 0.002% triton X-100, 10% methanol, and 4% PEG.

BUFFER 7: Reagents are mixed together to form a 10X stock solution of buffer 6 (400 mM Tris-Cl (pH 8.0), 120 mM $MgCl_2$, 50 mM DTT, 10 mM spermidine and 0.02% triton X-100. Prior to initiation of the polymerase reaction PEG, methanol

20   and LiCl is added and the buffer is diluted such that the final reaction conditions for buffer 6 consisted of : 40mM tris pH (8.0), 12 mM $MgCl_2$, 5 mM DTT, 1 mM spermidine, 0.002% triton X-100, 10% methanol, 4% PEG, and 1 mM LiCl.

Example 4: Screening of Modified nucleotide triphosphates with Mutant T7 RNA Polymerase

25   Each modified nucleotide triphosphate was individully tested in buffers 1 through 6 at two different temperatures (25 and 37°C). Buffers 1-6 tested at 25°C were designated conditions 1-6 and buffers 1-6 test at 37°C were designated conditions 7-12 (table 3). In each condition, Y639F mutant T7 polymerase (Sousa and Padilla, *Supra*) (0.3-2 mg/20 ml reaction), NTP's (2 mM each), DNA template

30   (10 pmol), inorganic pyrophosphatase (5U/ml) and α-^{32}P NTP(0.8 mCi/pmol template) were combined and heated at the designated temperatures for 1-2 hours. The radiolabeled NTP used was different from the modified triphosphate being testing. The samples were resolved by polyacrylamide gel electrophoresis. Using a phosphorImager (Molecular Dynamics, Sunnyvale, CA), the amount of full-length

transcript was quantified and compared with an all-RNA control reaction. The data is presented in **Table 4**; results in each reaction is expressed as a percent compared to the all-ribonucleotide triphosphate (rNTP) control. The control was run with the mutant T7 polymerase using commercially available polymerase buffer (Boehringer Mannheim, Indianapolis, IN).

Example 5: Incorporation of Modified NTP's using Wild-type T7 RNA polymerase

Bacteriophage T7 RNA polymerase was purchased from Boehringer Mannheim at 0.4 U/μL concentration. Applicant used the commercial buffer supplied with the enzyme and 0.2 μCi alpha-^{32}P NTP in a 50 μL reaction with nucleotides triphosphates at 2 mM each. The template was double-stranded PCR fragment, which was used in previous screens. Reactions were carried out at 37°C for 1 hour. 10 μL of the sample was run on a 7.5% analytical PAGE and bands were quantitated using a PhosphorImager. Results are calculated as a comparison to an "all ribo" control (non-modified nucleotide triphosphates) and the results are in Table 5.

EXAMPLE 6: Incorporation of Multiple Modified nucleotide triphosphates Into Oligonucleotides

Combinations of modified nucleotide triphosphates were tested with the transcription protocol described in example 4, to determine the rates of incorporation of two or more of these triphosphates. Incorporation 2'-Deoxy-2'-(L-histidine) amino uridine (2'-his-NH_2-UTP) was tested with unmodified cytidine nucleotide triphosphates, rATP and rGTP in reaction condition number 9. The data is presented as a percentage of incorporation of modified NTP's compared to the all rNTP control and is shown in **Table 6a**.

Two modified cytidines (2'-NH_2-CTP or 2'dCTP) were incorporated along with 2'-his-NH_2-UTP with identical efficiencies. 2'-his-NH_2-UTP and 2'-NH_2-CTP were then tested with various unmodified and modified adenosine triphosphates in the same buffer (**Table 6b**). The best modified adenosine triphosphate for incorporation with both 2'-his-NH_2-UTP and 2'-NH_2-CTP was 2'-NH_2-DAPTP.

EXAMPLE 7: Optimization of Reaction conditions for Incorporation of Modified Nucleotide Triphosphate

The combination of 2'-his-NH$_2$-UTP, 2'-NH$_2$-CTP, 2'-NH$_2$-DAP, and rGTP was tested in several reaction conditions (**Table 7**) using the incorporation protocol described in example 9. The results demonstrate that of the buffer conditions tested, incorporation of these modified nucleotide triphosphates occur in the presence of both methanol and LiCl.

Example 8: Selection of Novel Enzymatic nucleic acid molecule Motifs using 2'-deoxy-2'amino Modified GTP and CTP

For selection of new enzymatic nucleic acid molecule motifs, pools of enzymatic nucleic acid molecule were designed to have two substrate binding arms (5 and 16 nucleotides long) and a random region in the middle. The substrate has a biotin on the 5' end, 5 nucleotides complementary to the short binding arm of the pool, an unpaired G (the desired cleavage site), and 16 nucleotides complementary to the long binding arm of the pool. The substrate was bound to column resin through an avidin-biotin complex. The general process for selection is shown in figure 2. The protocols described below represent one possible method which may be utilized for selection of enzymatic nucleic acid molecules and are given as a non-limiting example of enzymatic nucleic acid molecule selection with combinatorial libraries.

Construction of Libraries: The oligonucleotides listed below were synthesized by Operon Technologies (Alameda, CA). Templates were gel purified and then run through a Sep-Pak cartridge (Waters, Millford, MA) using the manufacturers protocol. Primers (MST3, MST7c, MST3del) were used without purification.

Primers:

MST3 (30 mer): 5'- CAC TTA GCA TTA ACC CTC ACT AAA GGC CGT-3'

MST7c (33 mer): 5'-TAA TAC GAC TCA CTA TAG GAA AGG TGT GCA ACC-3'

MST3del (18 mer): 5'-ACC CTC ACT AAA GGC CGT-3'

Templates:

MSN60c (93 mer): 5'-ACC CTC ACT AAA GGC CGT (N)$_{60}$ GGT TGC ACA CCT TTG-3'

MSN40c (73 mer): 5'-ACC CTC ACT AAA GGC CGT (N)$_{40}$ GGT TGC ACA CCT TTG-3'

MSN20c (53 mer): 5'-ACC CTC ACT AAA GGC CGT (N)$_{20}$ GGT TGC ACA CCT TTG-3'

N60 library was constructed using MSN60c as a template and MST3/MST7c as primers. N40 and N20 libraries were constructed using MSN40c (or MSN20c) as template and MST3del/MST7c as primers.

Single stranded templates were were converted into double-stranded DNA by the following protocol: 5 nmol template, 10 nmol each primer, in 10 ml reaction volume using standard PCR buffer, dNTP's, and taq DNA polymerase (all reagents from Boerhinger Mannheim). Synthesis cycle conditions were 94°C, 4 minutes; (94°C, 1minute; 42°C, 1 minute; 72°C, 2 minutes) x 4; 72°C, 10 minutes. Products were checked on agarose gel to confirm the length of each fragment (N60=123 bp, N40=91 bp, N20=71 bp) and then were phenol/chloroform extracted and ethanol precipitated. Concentration of the double-stranded product was 25 μM.

Transcription of the initial pools was performed in a 1 ml volume comprising: 500 pmol double-stranded template (3 x 10^{14} molecules), 40 mM tris-HCl (pH 8.0), 12 mM MgCl$_2$, 1 mM spermidine, 5 mM DTT, 0.002% triton X-100, 1 mM LiCl, 4% PEG 8000, 10% methanol, 2 mM ATP (Pharmacia), 2 mM GTP (Pharmacia), 2 mM 2'-deoxy-2'-amino-CTP (USB), 2 mM 2'-deoxy-2'-amino-UTP (USB), 5 U/ml inorganic pyrophosphatase (Sigma), 5 U/μl T7 RNA polymerase (USB; Y639F mutant was used in some cases at 0.1 mg/ml (Sousa and Padilla, *Supra*)), 37°C, 2 hours. Transcribed libraries were purified by denaturing PAGE (N60=106 ntds, N40=74, N20=54) and the resulting product was desalted using Sep-Pak columns and then ethanol precipitated.

<u>Initial column-Selection</u>: The following biotinylated substrate was synthesized using standard protocols (Usman *et al.*, 1987 *J. Am. Chem. Soc.*, 109, 7845; Scaringe *et al.*, 1990 *Nucleic Acids Res.*, 18, 5433; and Wincott *et al.*, 1995 *Nucleic Acids Res.* 23, 2677-2684):

5'-biotin-C18 spacer-GCC GUG GGU UGC ACA CCU UUC C-C18 spacer-thiol-modifier C6 S-S-inverted abasic-3'

Substrate was purified by denaturing PAGE and ethanol precipitated. 10 nmol of substrate was linked to a NeutrAvidin column using the following protocol: 400 μl UltraLink Immobilized NeutrAvidin slurry (200 μl beads, Pierce, Rockford, IL) were loaded into a polystyrene column (Pierce). The column was washed twice with 1 ml of binding buffer (20 mM $NaPO_4$ (pH 7.5), 150 mM NaCl) and then capped off (i.e., a cap was put on the bottom of the column to stop the flow). 200 μl of the substrate suspended in binding buffer was applied and allowed to incubate at room temperature for 30 minutes with occasional vortexing to ensure even linking and distribution of the solution to the resin. After the incubation, the cap was removed and the column was washed with 1 ml binding buffer followed by 1 ml column buffer (50 mM tris-HCL (pH 8.5), 100 mM NaCl, 50 mM KCl). The column was then ready for use and capped off. 1 nmol of the initial pool RNA was loaded on the column in a volume of 200 μl column buffer. It was allowed to bind the substrate by incubating for 30 minutes at room temperature with occasional vortexing. After the incubation, the cap was removed and the column was washed twice with 1 ml column buffer and capped off. 200 μl of elution buffer (50 mM tris-HCl (pH 8.5), 100 mM NaCl, 50 mM KCl, 25 mM $MgCl_2$) was applied to the column followed by 30 minute incubation at room temperature with occasional vortexing. The cap was removed and four 200 μl fractions were collected using elution buffer.

Second column (counter selection): A diagram for events in the second column is generally shown in figure 3 and substrate oligonucleotide used is shown below:

5'-GGU UGC ACA CCU UUC C-C18 spacer-biotin-inverted abasic-3'

This column substrate was linked to UltraLink NeutrAvidin resin as previously described (40 pmol) which was washed twice with elution buffer. The eluent from the first column purification was then run on the second column. The use of this column allowed for binding of RNA that non-specifically diluted from the first column, while RNA that performed a catalytic event and had product bound to it, flowed through the second column. The fractions were ethanol precipitated using glycogen as carrier and rehydrated in sterile water for amplification.

Amplification: RNA and primer MST3 (10-100 pmol) were denatured at 90°C for 3 minutes in water and then snap-cooled on ice for one minute. The following reagents were added to the tube (final concentrations given): 1X PCR buffer (Boerhinger Mannheim), 1 mM dNTP's (for PCR, Boerhinger Mannheim), 2 U/μl

RNase-Inhibitor (Boerhinger Mannheim), 10 U/µl Superscript II Reverse Transcriptase (BRL). The reaction was incubated for 1 hour at 42°C, then at 95°C for 5 minutes in order to destroy the Superscript. The following reagents were then added to the tube to increase the volume five-fold for the PCR step (final concentrations/amounts given): MST7c primer (10-100 pmol, same amount as in RT step), 1X PCR buffer, taq DNA polymerase (0.025-0.05 U/µl, Boerhinger Mannheim). The reaction was cycled as follows: 94°C, 4minutes; (94°C, 30s; 42-54°C, 30s; 72°C, 1minute) x 4-30 cycles; 72°C, 5minutes; 30°C, 30 minutes. Cycle number and annealing temperature were decided on a round by round basis. In cases where heteroduplex was observed, the reaction was diluted five-fold with fresh reagents and allowed to progress through 2 more amplification cycles. Resulting products were analyzed for size on an agarose gel (N60=123 bp, N40=103 bp, N20=83 bp) and then ethanol precipitated.

Transcriptions: Transcription of amplified products was done using the conditions described above with the following modifications: 10-20% of the amplification reaction was used as template, reaction volume was 100-500 µl, and the products sizes varied slightly (N60=106 ntds, N40=86, N20=66). A small amount of ^{32}P-GTP was added to reactions for quantitation purposes.

Subsequent rounds: Subsequent rounds of selection used 20 pmols of input RNA and 40 pmol of the 22 nucleotide substrate on the column.

Activity of pools: Pools were assayed for activity under single turnover conditions every three to four rounds. Activity assay conditions were as follows: 50 mM tris-HCl (pH 8.5), 25 mM MgCl$_2$, 100 mM NaCl, 50 mM KCl, trace ^{32}P labeled substrate, 10 nM RNA pool. 2X pool in buffer and, separately, 2X substrate in buffer were incubated at 90°C for 3 minutes, then at 37°C for 3 minutes. Equal volume 2X substrate was then added the 2X pool tube (t=0). Initial assay time points were taken at 4 and 24 hours: 5 µl was removed and quenched in 8 µl cold Stop buffer (96% formamide, 20 mM EDTA, 0.05% bromphenyl blue/xylene cyanol). Samples were heated 90°C, 3 minutes, and loaded on a 20% sequencing gel. Quantitation was performed using a Molecular Dynamics Phosphorimager and ImageQuaNT software. The data is shown in table 8.

Samples from the pools of oligonucleotide were cloned into vectors and sequenced using standard protocols (Sambrook *et al., Molecular Cloning: A Laboratory Manual*, Cold Spring Harbor Laboratory Press). The enzymatic nucleic

acid molecules were transcribed from a representative number of these claones using methods described in this application. Individuals from each pool were tested for RNA cleavage from N60 and N40 by incubating the enzymatic nucleic acid molecules from the clones with 5/16 substrate in 2mM MgCl2, pH 7.5, 10mM KCl at 37°C. The data in table 10 shows that the enzymatic nucleic acid molecules isolated from the pool are individually active.

Kinetic Activity: Kinetic activity of the enzymatic nucleic acid molecule shown in table 10, was determined by incubating enzymatic nucleic acid molecule (10 nM) with substrate in a cleavage buffer (pH 8.5, 25 mM $MgCl_2$, 100 mM NaCl, 50 mM KCl) at 37°C.

Magnesium Dependence: Magnesium dependence of round 15 of N20 was tested by varying $MgCl_2$ while other conditions were held constant (50 mM tris pH 8.0, 100 mM NaCl, 50 mM KCl, single turnover, 10 nM pool). The data is shown in table 11, which demonstrates increased activity with increased magnesium concentrations.

Example 9: Selection of Novel Enzymatic nucleic acid molecule Motifs using 2'-Deoxy-2'-(N-histidyl) amino UTP, 2'-Fluoro-ATP, and 2'-deoxy-2'-amino CTP and GTP

The method described in example 8 was repeated using 2'-Deoxy-2'-(N-histidyl) amino UTP, 2'-Fluoro-ATP, and 2'-deoxy-2'-amino CTP and GTP. However, rather than causing cleavage on the initial column with $MgCl_2$, the initial random modified-RNA pool was loaded onto substrate-resin in the following buffer; 5 mM NaoAc pH 5.2, 1 M NaCl at 4° C. After ample washing the resin was moved to 22 ° C and the buffer switch 20 mM HEPES pH 7.4, 140 mM KCl, 10 mM NaCl, 1 mM $CaCl_2$, 1 mM $MgCl_2$. In one selection of N60 oligonucleotides, no divalent cations ($MgCl_2$, $CaCl_2$) was used. The resin was incubated for 10 minutes to allow reaction and the eluant collected.

The enzymatic nucleic acid molecule pools were capable of cleaving 1-3% of the present substrate even in the absense of divalent cations, the background (in the absence of modified pools) was 0.2 - 0.4 %.

Example 10: Synthesis of 5-Imidazoleacetic acid 2'-deoxy-5'-triphosphate uridine

5-dintrophenylimidazoleacetic acid 2'-deoxy uridine nucleoside (80 mg) was dissolved in 5 ml of triethylphosphate while stirring under argon, and the reaction mixture was cooled to 0°C. Phosphorous oxychloride (1.8 eq, 22 ml) was added to the reaction mixture at 0°C, three more aliquots were added over the course of 48 hours at room temperature. The reaction mixture was then diluted with anhydrous MeCN (5 ml) and cooled to 0°C,followed by the addition of tributylamine (0.65 ml) and tributylammonium pyrophosphate (4.0 eq, 0.24 g). After 45 minutes, the reaction was quenched with 10 ml aq. methyl amine for four hours. After co-evaporation with MeOH (3x), purified material on DEAE Sephadex followed by RP chromatography to afford 15 mg of triphosphate.

Example 11:Synthesis of 2'-(N-lysyl) amino -2'-deoxy-cytidine Triphosphate

2'-(N-lysyl)amino 2'-deoxy cytidine (0.180 g, 0.22 mmol) was dissolved in triethyl phosphate (2.00 ml) under Ar. The solution was cooled to 0 °C in an ice bath. Phosphorus oxychloride (99.999%, 3 eq., 0.0672 mL) was added to the solution and the reaction was stirred for two hours at 0 °C. Tributylammonium pyrophosphate (4 eq., 0.400 g) was dissolved in 3.42 mL of acetonitrile and tribuytylamine (0.165 mL). Acetonitrile (1 mL) was added to the monophosphate solution followed by the pyrophosphate solution which was added dropwise. The solution was clear. The reaction was allowed to warm up to room temperature. After stirring for 45 minutes, methyl amine (5 mL) was added and the reaction and stirred at room temperature for 2 hours. A two phase mixture appeared (little beads at the bottom of the flask). TLC (7:1:2 iPrOH:NH4OH:H2O) showed the appearance of a triphosphate material. The solution was concentrated, dissolved in water and loaded on a newly prepared DEAE Sephadex A-25 column. The column was washed with a gradiant up to 0.6 M TEAB buffer and the product eluted off in fractions 90-95. The fractions were analyzed by ion exchange HPLC. Each fraction showed one triphosphate peak that eluted at ~4.000 minutes. The fractions were combined and pumped down from methanol to remove buffer salt to yield 15.7 mgs of product.

Example 12: Synthesis of 2'-Deoxy -2'-(L-histidine)amino Cytidine Triphosphate

2'-[N-Fmoc, N^{imid} -dinitrophenyl-histidyl]amino-2'-cytidine (0.310 g, 4.04 mmol) was dissolved in triethyl phosphate (3 ml) under Ar. The solution was cooled to 0 °C. Phosphorus oxychloride (1.8 eq., 0.068 mL) was added to the solution and stored overnight in the freezer. The next morning TLC (10% MeOH in CH2Cl2)

showed a lot of starting material, so one more equivalent of $POCl_3$ was added. After two hours the TLC still showed starting material. Tributylamine (0.303 mL) and Tributylammonium pyrophosphate (4 eq., 0.734 g) dissolved in 6.3 mL of acetonitrile (added dropwise) were added to the monophosphate solution. The reaction was allowed to warm up to room temperature. After stirring for 15 min methyl amine (10 mL) was added at room temperature and stirring continued for 2 hours. TLC (7:1:2 iPrOH:NH$_4$OH:H$_2$O) showed the appearance of a triphosphate material. The solution was concentrated, dissolved in water and loaded on a DEAE Sephadex A-25 column. The column was washed with a gradiant up to 0.6 M TEAB buffer and the product eluted off in fractions 170-179. The fractions were analyzed by ion exchange HPLC. Each fraction showed one triphosphate peak that eluted at ~6.77 minutes. The fractions were combined and pumped down from methanol to remove buffer salt to aford 17 mgs of product.

Example 13: Screening for Novel Enzymatic nucleic acid molecule Motifs Using Modified NTPs (Class I Motif)

Our initial pool contained 3×10^{14} individual sequences of 2'-amino-dCTP/2'-amino-dUTP RNA. We optimized transcription conditions in order to increase the amount of RNA product by inclusion of methanol and lithium chloride. 2'-amino deoxynucleotides do not interfere with the reverse transcription and amplification steps of selection and confer nuclease resistance. We designed the pool to have two binding arms complementary to the substrate, separated by the random 40 nucleotide region. The 16-mer substrate had two domains, 5 and 10 nucleotides long, that bind the pool, separated by an unpaired guanosine. On the 5' end of the substrate was a biotin attached by a C18 linker. This enabled us to link the substrate to a NeutrAvidin resin in a column format. The desired reaction would be cleavage at the unpaired G upon addition of magnesium cofactor followed by dissociation from the column due to instability of the 5 base pair helix. A detailed protocol follows:

Enzymatic nucleic acid molecule Pool Prep: The initial pool DNA was prepared by converting the following template oligonucleotides into double-stranded DNA by filling in with taq polymerase. (template=5'-ACC CTC ACT AAA GGC CGT (N)$_{40}$ GGT TGC ACA CCT TTC-3'; primer 1=5'- CAC TTA GCA TTA ACC CTC ACT AAA GGC CGT-3'; primer 2=5'-TAA TAC GAC TCA CTA TAG GAA AGG TGT GCA ACC-3'.) All DNA oligonucleotides were synthesized by Operon technologies. Template oligos were purified by denaturing PAGE and Sep-pak chromatography columns (Waters). RNA substrate oligos were using standard solid

phase chemistry and purified by denaturing PAGE followed by ethanol precipitation. Substrates for *in vitro* cleavage assays were 5'-end labeled with gamma-^{32}P-ATP and T4 polynucleotide kinase followed by denaturing PAGE purification and ethanol precipitation.

5   5 nmole of template, 10 nmole of each primer and 250 U taq polymerase were incubated in a 10 ml volume with 1X PCR buffer (10 mM tris-HCl (pH 8.3), 1.5 mM MgCl$_2$, 50 mM KCl) and 0.2 mM each dNTP as follows: 94°C, 4 minutes; (94°C, 1 min; 42°C, 1 min; 72°C, 2 min) through four cycles; and then 72°C, for 10 minutes. The product was analyzed on 2% Separide agarose gel for size and then

10   was extracted twice with buffered phenol, then chloroform-isoamyl alcohol, and ethanol precipitated. The initial RNA pool was made by transcription of 500 pmole (3 x 10^{14} molecules) of this DNA as follows. Template DNA was added to 40 mM tris-HCl (pH 8.0), 12 mM MgCl$_2$, 5 mM dithiothreitol (DTT), 1 mM spermidine, 0.002% triton X-100, 1 mM LiCl, 4% PEG-8000, 10% methanol, 2 mM ATP, 2 mM

15   GTP, 2 mM 2'-amino-dCTP, 2 mM 2'-amino-dUTP, 5 U/ml inorganic pyrophosphatase, and 5 U/μl T7 RNA polymerase at room temperature for a total volume of 1 ml. A separate reaction contained a trace amount of alpha-^{32}P-GTP for detection. Transcriptions were incubated at 37°C for 2 hours followed by addition of equal volume STOP buffer (94% formamide, 20 mM EDTA, 0.05% bromophenol

20   blue). The resulting RNA was purified by 6% denaturing PAGE gel, Sep-pak chromatography, and ethanol precipitated.

       INITIAL SELECTION: 2 nmole of 16 mer 5'-biotinylated substrate (5'-biotin-C18 linker-GCC GUG GGU UGC ACA C-3') was linked to 200 μl UltraLink Immobilized NeutrAvidin resin (400 μl slurry, Pierce) in binding buffer (20 mM

25   NaPO$_4$ (pH 7.5), 150 mM NaCl) for 30 minutes at room temperature. The resulting substrate column was washed with 2 ml binding buffer followed by 2 ml column buffer (50 mM tris-HCl (pH 8.5), 100 mM NaCl, 50 mM KCl). The flow was capped off and 1000 pmole of initial pool RNA in 200 μl column buffer was added to the column and incubated 30 minutes at room temperature. The column was

30   uncapped and washed with 2 ml column buffer, then capped off. 200 μl elution buffer (=column buffer + 25 mM MgCl$_2$) was added to the column and allowed to incubate 30 minutes at room temperature. The column was uncapped and eluent collected followed by three 200 μl elution buffer washes. The eluent/washes were ethanol precipitated using glycogen as carrier and rehydrated in 50 μl sterile H$_2$O.

35   The eluted RNA was amplified by standard reverse transcription/PCR amplification techniques. 5-31 μl RNA was incubated with 20 pmol of primer 1 in 14 μl volume

90° for 3 min then placed on ice for 1 minute. The following reagent were added (final concentrations noted): 1X PCR buffer, 1 mM each dNTP, 2 U/µl RNase Inhibitor, 10 U/µl SuperScript II reverse transcriptase. The reaction was incubated 42° for 1 hour followed by 95° for 5 min in order to inactivate the reverse transcriptase. The volume was then increased to 100 µl by adding water and reagents for PCR: 1X PCR buffer, 20 pmol primer 2, and 2.5 U taq DNA polymerase. The reaction was cycled in a Hybaid thermocycler: 94°, 4 min; (94°C, 30 sec; 54°C, 30 sec; 72°C, 1 min) X 25; 72°C, 5 min. Products were analyzed on agarose gel for size and ethanol precipitated. One-third to one-fifth of the PCR DNA was used to transcribe the next generation, in 100 µl volume, as described above. Subsequent rounds used 20 pmol RNA for the column with 40 pmol substrate.

TWO COLUMN SELECTION: At generation 8 (G8), the column selection was changed to the two column format. 200 pmoles of 22 mer 5'-biotinylated substrate (5'-biotin-C18 linker-GCC GUG GGU UGC ACA CCU UUC C-C18 linker-thiol modifier C6 S-S-inverted abasic-3') was used in the selection column as described above. Elution was in 200 µl elution buffer followed by a 1 ml elution buffer wash. The 1200 µl eluent was passed through a product trap column by gravity. The product trap column was prepared as follows: 200 pmol 16 mer 5'-biotinylated "product" (5'-GGU UGC ACA CCU UUC C-C18 linker-biotin-3') was linked to the column as described above and the column was equilibrated in elution buffer. Eluent from the product column was precipitated as previously described. The products were amplified as above only with 2.5-fold more volume and 100 pmol each primer. 100 µl of the PCR reaction was used to do a cycle course; the remaining fraction was amplified the minimal number of cycles needed for product. After 3 rounds (G11), there was visible activity in a single turnover cleavage assay. By generation 13, 45% of the substrate was cleaved at 4 hours; k_{obs} of the pool was 0.037 min^{-1} in 25 mM MgCl$_2$. We subcloned and sequenced generation 13; the pool was still very diverse. Since our goal was a enzymatic nucleic acid molecule that would work in a physiological environment, we decided to change selection pressure rather than exhaustively catalog G13.

Reselection of the N40 pool was started from G12 DNA. Part of the G12 DNA was subjected to hypermutagenic PCR (Vartanian *et al.*, 1996, *Nucleic Acids Research* 24, 2627-2631) to introduce a 10% per position mutation frequency and was designated N40H. At round 19, part of the DNA was hypermutagenized again, giving N40M and N40HM (a total of 4 parallel pools). The column substrates

37

remained the same; buffers were changed and temperature of binding and elution was raised to 37°C. Column buffer was replaced by physiological buffer (50 mM tris-HCl (pH 7.5), 140 mM KCl, 10 mM NaCl) and elution buffer was replaced by 1 mM Mg buffer (physiological buffer + 1 mM $MgCl_2$). Amount of time allowed for the pool to bind the column was eventually reduced to 10 min and elution time was gradually reduced from 30 min to 20 sec. Between rounds 18 and 23, k_{obs} for the N40 pool stayed relatively constant at 0.035-0.04 min^{-1}. Generation 22 from each of the 4 pools was cloned and sequenced.

CLONING AND SEQUENCING: Generations 13 and 22 were cloned using Novagen's Perfectly Blunt Cloning kit (pT7Blue-3 vector) following the kit protocol. Clones were screened for insert by PCR amplification using vector-specific primers. Positive clones were sequenced using ABI Prism 7700 sequence detection system and vector-specific primer. Sequences were aligned using MacVector software; two-dimensional folding was done using Mulfold software (Zuker,, 1989, *Science* 244, 48-52; Jaeger *et al.*, 1989, *Biochemistry* 86, 7706-7710; Jaeger *et al.*, 1989, R. F. Doolittle ed., *Methods in Enzymology*, 183, 281-306). Individual clone transcription units were constructed by PCR amplification with 50 pmol each primer 1 and primer 2 in 1X PCR buffer, 0.2 mM each dNTP, and 2.5 U of taq polymerase in 100 µl volume cycled as follows: 94°C, 4 min; (94°C, 30 sec; 54°C, 30 sec; 72°C, 1 min) X 20; 72°C, 5 min. Transcription units were ethanol precipitated, rehydrated in 30 µl H2O, and 10 µl was transcribed in 100 µl volume and purified as previously described.

Thirty-six clones from each pool were sequenced and were found to be variations of the same consensus motif. Unique clones were assayed for activity in 1 mM $MgCl_2$ and physiological conditions; nine clones represented the consensus sequence and was used in subsequent experiments. There were no mutations that significantly increased activity; most of the mutations were in regions believed to be duplex, based on the proposed secondary structure. In order to make the motif shorter, we deleted the 3'-terminal 25 nucleotides necessary to bind the primer for amplification. The measured rates of the full length and truncated molecules were both 0.04 min^{-1}; thus we were able reduce the size of the motif from 86 to 61 nucleotides. The molecule was shortened even further by truncating base pairs in the stem loop structures as well as the substrate recognition arms to yield a 48 nucleotide molecule. In addition many of the ribonucleotides were replaced with 2-O-methyl modified nucleotides to stabilize the molecule. An example of the new motif is given in figure 4. Those of ordinary skill in the art will recognize that the

molecule is not limited to the chemical modifications shown in the figure and that it represents only one possible chemically modified molecule.

KINETIC ANALYSIS

Single turnover kinetics were performed with trace amounts of 5'-^{32}P-labeled substrate and 10-1000 nM pool of enzymatic nucleic acid molecule. 2X substrate in 1X buffer and 2X pool/enzymatic nucleic acid molecule in 1X buffer were incubated separately 90° for 3 min followed by equilibration to 37° for 3 min. Equal volume of 2X substrate was added to pool/enzymatic nucleic acid molecule at t_0 and the reaction was incubated at 37°C. Time points were quenched in 1.2 vol STOP buffer on ice. Samples were heated to 90°C for 3 min prior to separation on 15% sequencing gels. Gels were imaged using a PhosphorImager and quantitated using ImageQuant software (Molecular Dynamics). Curves were fit to double-exponential decay in most cases, although some of the curves required linear fits.

STABILITY: Serum stability assays were performed as previously described (Beigelman *et al.*, 1995, *J. Biol. Chem.* 270, 25702-25708). 1 µg of 5'-32P-labeled synthetic enzymatic nucleic acid molecule was added to 13 µl cold and assayed for decay in human serum. Gels and quantitation were as described in kinetics section.

Example 14: Inhibition of HCV Using New Motif

During HCV infection, viral RNA is present as a potential target for enzymatic nucleic acid molecule cleavage at several processes: uncoating, translation, RNA replication and packaging. Target RNA may be more or less accessible to enzymatic nucleic acid molecule cleavage at any one of these steps. Although the association between the HCV initial ribosome entry site (IRES) and the translation apparatus is mimicked in the HCV 5'UTR/luciferase reporter system (example 9), these other viral processes are not represented in the OST7 system. The resulting RNA/protein complexes associated with the target viral RNA are also absent. Moreover, these processes may be coupled in an HCV-infected cell which could further impact target RNA accessibility. Therefore, we tested whether enzymatic nucleic acid molecules designed to cleave the HCV 5'UTR could effect a replicating viral system.

Recently, Lu and Wimmer characterized an HCV-poliovirus chimera in which the poliovirus IRES was replaced by the IRES from HCV (Lu & Wimmer, 1996, *Proc. Natl. Acad. Sci. USA*. 93, 1412-1417). Poliovirus (PV) is a positive strand RNA virus like HCV, but unlike HCV is non-enveloped and replicates

efficiently in cell culture. The HCV-PV chimera expresses a stable, small plaque phenotype relative to wild type PV.

The capability of the new enzymatic nucleic acid molecule motif to inhibit HCV RNA intracellularly was tested using a dual reporter system that utilizes both firefly and Renilla luciferase (figure 5). A number of enzymatic nucleic acid molecules having the new class I motif were designed and tested (Table XII). The new enzymatic nucleic acid molecule motif targeted to the 5' HCV UTR region, which when cleaved, would prevent the translation of the transcript into luciferase. OST-7 cells were plated at 12,500 cells per well in black walled 96 well plates (Packard) in medium DMEM containing 10% fetal bovine serum, 1% pen/strep, and 1% L-glutamine and incubated at 37°C overnight. A plasmid containing T7 promoter expressing 5' HCV UTR and firefly luciferase (T7C1-341 (Wang *et al.*, 1993, *J. of Virol.* 67, 3338-3344)) was mixed with a pRLSV40 Renilla control plasmid (Promega Corporation) followed by enzymatic nucleic acid molecule, and cationic lipid to make a 5X concentration of the reagents (T7C1-341 (4 μg/ml), pRLSV40 renilla luciferase control (6 μg/ml), enzymatic nucleic acid molecule (250 nM), transfection reagent (28.5 μg/ml).

The complex mixture was incubated at 37°C for 20 minutes. The media was removed from the cells and 120 μl of Opti-mem media was added to the well followed by 30 μl of the 5X complex mixture. 150 μl of Opti-mem was added to the wells holding the untreated cells. The complex mixture was incubated on OST-7 cells for 4 hours, lysed with passive lysis buffer (Promega Corporation) and luminescent signals were quantified using the Dual Luciferase Assay Kit using the manufacturer's protocol (Promega Corporation). The data shown in figure 6 is a dose curve of enzymatic nucleic acid molecule targeting site 146 of the HCV RNA and is presented as a ratio between the firefly and Renilla luciferase fluorescence. The enzymatic nucleic acid molecule was able to reduce the quantity of HCV RNA at all enzymatic nucleic acid molecule concentrations yielding an IC 50 of approximately 5 nM. Other sites were also efficacious (figure 7), in particular enzymatic nucleic acid molecules targeting 133, 209, and 273 were also able to reduce HCV RNA compared to the irrelevant (IRR) controls.

Example 15: Cleavage of Substrates Using Completely Modified Oligonucleotides

The ability of an enzymatic nucleic acid which is modified at every 2' position to cleave a target RNA was tested to determine if any ribonucleotide

positions are necessary. A ribozyme was constructed with 2'-O-methyl, and 2'-amino (NH$_2$) modified nucleotides (table 12; gene name: no ribo) and kinetic analysis was performed as described in example 13. 100 nM enzymatic nucleic acid was mixed with trace amounts of substrate in the presence of 1 mM MgCl$_2$ at physiological conditions (37°C). The no ribo nucleotide have a K$_{rel}$ of 0.13 compared to the enzymatic nucleic acid shown in table 12 (ribo) which contained ribonucleotides.

Example 16: Screening for Novel Enzymatic nucleic acid molecule Motifs (Class II Motifs)

The selections were initiated with pools of $> 10^{14}$ modified RNA's of the following sequence: 5'-GGGAGGAGGAAGUGCCU (N)$_{35}$ UGCCGCGCUCGCUCCCAGUCC-3'. The RNA was enzymatically generated using the mutant T7 Y639F RNA polymerase prepared by Rui Souza. The following modified NTP's were incorporated: 2'-deoxy-2'-fluoro-adenine triphosphate, 2'-deoxy-2'-fluoro-uridine triphosphate or 2'-deoxy-2'-fluoro-5-[(N-imidazole-4acetyl)propyl amine] uridine triphosphate, and 2'-deoxy-2'-amino-cytidine triphosphate; natural guanidine triphosphate was used in all selections so that alpha $-^{32}$P- GTP could be used to label pool RNA's. RNA pools were purified by denaturing gel electrophoresus 8% polyacrilamide 7 M Urea.

The following target RNA (resin A) was synthesized and coupled to Iodoacetyl Ultralink resin (Pierce) by the supplier's proceedure:5' –b-L-GGACUGGGAGCGAGCGCGGCGCAGGCACU GAAG-L-S-B-3'; where b is biotin (Glenn Research cat# 10-1953-nn), L is polyethylene glycol spacer (Glenn Research cat# 10-1918-nn), S is thiol-modifier C6 S-S (Glenn Research cat# 10-1936-nn), B is a standard inverted deoxy abasic.

RNA pools were added to 100 ul of 5 uM Resin A in the buffer A (20 mM HEPES pH 7.4, 140 mM KCL, 10 mM NaCl) and incubated at 22°C for 5 minutes. The temperature was then raised to 37°C for 10 minutes. The resin was washed with 5 ml buffer A. Reaction was triggered by the addition of buffer B(20 mM HEPES pH 7.4, 140 mM KCL, 10 mM NaCl, 1 mM MgCl$_2$, 1 mM CaCl$_2$). Incubation proceeded for 20 minutes in the first generation and was reduced progressively to 1 minute in the final generations; with 13 total generations. The reaction eluant was collected in 5 M NaCl to give a final concentration of 2 M NaCl. To this was added 100 μl of 50% slurry Ultralink NeutraAvidin (Pierce), Binding of cleaved biotin

product to the avidin resin was allowed by 20 minute incubation at 22° C. The resin was subsequently washed with 5 ml of 20 mM HEPES pH 7.4, 2 M NaCl. Desired RNA's were removed by a 1.2 ml denaturing wash 1M NaCl, 10 M Urea at 94° C over 10 minutes. RNA's were double precipitated in 0.3 M sodium acetate to remove Cl⁻ ions inhibitory to reverse transcription. Standard protocols of reverse transcription and PCR amplification were performed. RNA's were again transcribed with the modified NTP's described above. After 13 generations cloning and sequencing provided 14 sequences which were able to cleave the target substrate. Six sequences were characterized to determine secondary structure and kinetic cleavage rates. The structures and kinetic data is given in figure 8. The sequences of eight other enzymatic nucleic acid molecule sequences are given in table XIII. Size, sequence, and chemical compositions of these molecules can be modified as described under example 13 and as well known in the art.

Nucleic Acid Catalyst Engineering

Sequence, chemical and structural variants of Class I and Class II enzymatic nucleic acid molecule can be engineered and re-engineered using the techniques shown in this application and known in the art. For example, the size of class I and class II enzymatic nucleic acid molecules can, be reduced or increased using the techniques known in the art (Zaug *et al.*, 1986, *Nature,* 324, 429; Ruffner *et al.*, 1990, *Biochem.*, 29, 10695; Beaudry *et al.*, 1990, *Biochem.*, 29, 6534; McCall *et al.*, 1992, *Proc. Natl. Acad. Sci., USA.*, 89, 5710; Long *et al.*, 1994, Supra; Hendry *et al.*, 1994, *BBA* 1219, 405; Benseler *et al.*, 1993, *JACS*, 115, 8483; Thompson *et al.*, 1996, *Nucl. Acids Res.*, 24, 4401;Michels *et al.*, 1995, *Biochem.*, 34, 2965; Been *et al.*, 1992, *Biochem.*, 31, 11843; Guo *et al.*, 1995, *EMBO. J.*, 14, 368; Pan *et al.*, 1994, *Biochem.*, 33, 9561; Cech, 1992, *Curr. Op. Struc. Bio.*, 2, 605; Sugiyama *et al.*, 1996, *FEBS Lett.*, 392, 215; Beigelman *et al.*, 1994, *Bioorg. Med. Chem.*, 4, 1715; Santoro *et al.*, 1997, *PNAS* 94, 4262; all are incorporated in its totality by reference herein), to the extent that the overall catalytic activity of the ribozyme is not significantly decreased.

Further rounds of *in vitro* selection strategies described herein and variations thereof can be readily used by a person skilled in the art to evolve additional nucleic acid catalysts and such new catalysts are within the scope of the instant invention.

Applications

The use of NTP's described in this invention have several research and commercial applications. These modified nucleotide triphosphates can be used for *in vitro* selection (evolution) of oligonucleotides with novel functions. Examples of *in vitro* selection protocols are incorporated herein by reference (Joyce, 1989, *Gene,* 82, 83-87; Beaudry *et al.,* 1992, *Science* 257, 635-641; Joyce, 1992, *Scientific American* 267, 90-97; Breaker *et al.,* 1994, *TIBTECH* 12, 268; Bartel *et al.,*1993, *Science* 261:1411-1418; Szostak, 1993, *TIBS* 17, 89-93; Kumar *et al.,* 1995, *FASEB J.,* 9, 1183; Breaker, 1996, *Curr. Op. Biotech.,* 7, 442).

Additionally, these modified nucleotide triphosphates can be employed to generate modified oligonucleotide combinatorial chemistry libraries. Several references for this technology exist (Brenner *et al.,* 1992, *PNAS* 89, 5381-5383, Eaton, 1997, *Curr. Opin. Chem. Biol.* 1, 10-16) which are all incorporated herein by reference.

Diagnostic uses

Enzymatic nucleic acid molecules of this invention may be used as diagnostic tools to examine genetic drift and mutations within diseased cells or to detect the presence of specific RNA in a cell. The close relationship between enzymatic nucleic acid molecule activity and the structure of the target RNA allows the detection of mutations in any region of the molecule which alters the base-pairing and three-dimensional structure of the target RNA. By using multiple enzymatic nucleic acid molecules described in this invention, one may map nucleotide changes which are important to RNA structure and function *in vitro*, as well as in cells and tissues. Cleavage of target RNAs with enzymatic nucleic acid molecules may be used to inhibit gene expression and define the role (essentially) of specified gene products in the progression of disease. In this manner, other genetic targets may be defined as important mediators of the disease. These experiments will lead to better treatment of the disease progression by affording the possibility of combinational therapies (e.g., multiple enzymatic nucleic acid molecules targeted to different genes, enzymatic nucleic acid molecules coupled with known small molecule inhibitors, radiation or intermittent treatment with combinations of enzymatic nucleic acid molecules and/or other chemical or biological molecules). Other in vitro uses of enzymatic nucleic acid molecules of this invention are well known in the art, and include detection of the presence of mRNAs associated with related conditions. Such RNA is detected by determining the presence of a cleavage

product after treatment with a enzymatic nucleic acid molecule using standard methodology.

In a specific example, enzymatic nucleic acid molecules which can cleave only wild-type or mutant forms of the target RNA are used for the assay. The first enzymatic nucleic acid molecule is used to identify wild-type RNA present in the sample and the second enzymatic nucleic acid molecule will be used to identify mutant RNA in the sample. As reaction controls, synthetic substrates of both wild-type and mutant RNA will be cleaved by both enzymatic nucleic acid molecules to demonstrate the relative enzymatic nucleic acid molecule efficiencies in the reactions and the absence of cleavage of the "non-targeted" RNA species. The cleavage products from the synthetic substrates will also serve to generate size markers for the analysis of wild-type and mutant RNAs in the sample population. Thus each analysis will require two enzymatic nucleic acid molecules, two substrates and one unknown sample which will be combined into six reactions. The presence of cleavage products will be determined using an RNAse protection assay so that full-length and cleavage fragments of each RNA can be analyzed in one lane of a polyacrylamide gel. It is not absolutely required to quantify the results to gain insight into the expression of mutant RNAs and putative risk of the desired phenotypic changes in target cells. The expression of mRNA whose protein product is implicated in the development of the phenotype is adequate to establish risk. If probes of comparable specific activity are used for both transcripts, then a qualitative comparison of RNA levels will be adequate and will decrease the cost of the initial diagnosis. Higher mutant form to wild-type ratios will be correlated with higher risk whether RNA levels are compared qualitatively or quantitatively.

Additional Uses

Potential usefulness of sequence-specific enzymatic nucleic acid molecules of the instant invention might have many of the same applications for the study of RNA that DNA restriction endonucleases have for the study of DNA (Nathans *et al.*, 1975 *Ann. Rev. Biochem.* 44:273). For example, the pattern of restriction fragments could be used to establish sequence relationships between two related RNAs, and large RNAs could be specifically cleaved to fragments of a size more useful for study. The ability to engineer sequence specificity of the enzymatic nucleic acid molecule is ideal for cleavage of RNAs of unknown sequence. Applicant describes the use of nucleic acid molecules to down-regulate gene expression of target genes

in bacterial, microbial, fungal, viral, and eukaryotic systems including plant, or mammalian cells.

All patents and publications mentioned in the specification are indicative of the levels of skill of those skilled in the art to which the invention pertains. All references cited in this disclosure are incorporated by reference to the same extent as if each reference had been incorporated by reference in its entirety individually.

One skilled in the art would readily appreciate that the present invention is well adapted to carry out the objects and obtain the ends and advantages mentioned, as well as those inherent therein. The methods and compositions described herein as presently representative of preferred embodiments are exemplary and are not intended as limitations on the scope of the invention. Changes therein and other uses will occur to those skilled in the art, which are encompassed within the spirit of the invention, are defined by the scope of the claims.

It will be readily apparent to one skilled in the art that varying substitutions and modifications may be made to the invention disclosed herein without departing from the scope and spirit of the invention. Thus, such additional embodiments are within the scope of the present invention and the following claims.

The invention illustratively described herein suitably may be practiced in the absence of any element or elements, limitation or limitations which is not specifically disclosed herein. Thus, for example, in each instance herein any of the terms "comprising", "consisting essentially of" and "consisting of" may be replaced with either of the other two terms. The terms and expressions which have been employed are used as terms of description and not of limitation, and there is no intention that in the use of such terms and expressions of excluding any equivalents of the features shown and described or portions thereof, but it is recognized that various modifications are possible within the scope of the invention claimed. Thus, it should be understood that although the present invention has been specifically disclosed by preferred embodiments, optional features, modification and variation of the concepts herein disclosed may be resorted to by those skilled in the art, and that such modifications and variations are considered to be within the scope of this invention as defined by the description and the appended claims.

In addition, where features or aspects of the invention are described in terms of Markush groups or other grouping of alternatives, those skilled in the art will
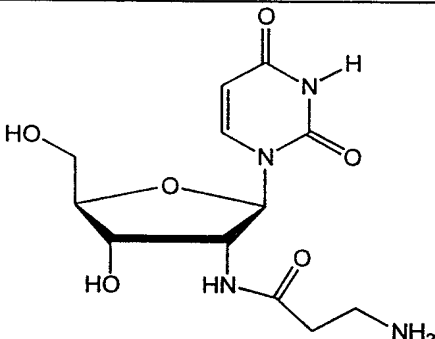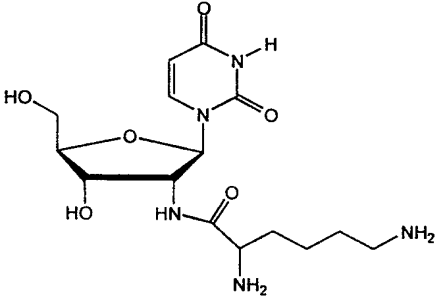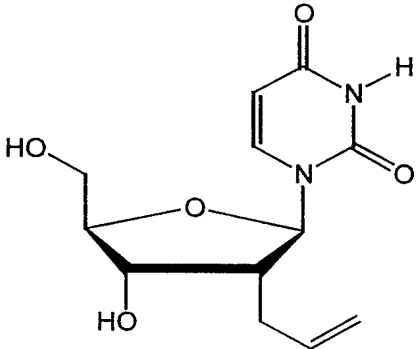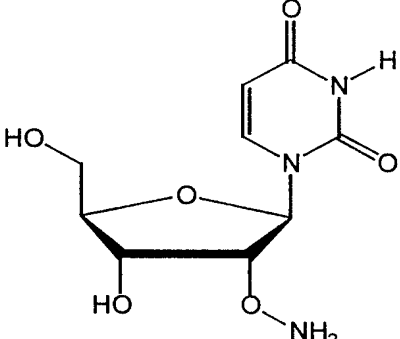
recognize that the invention is also thereby described in terms of any individual member or subgroup of members of the Markush group or other group.
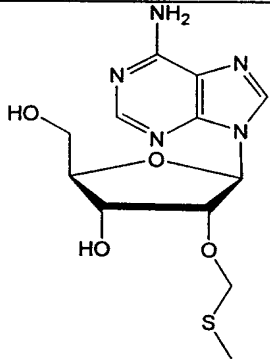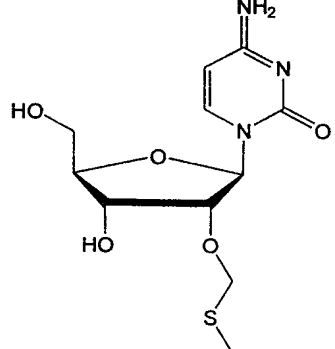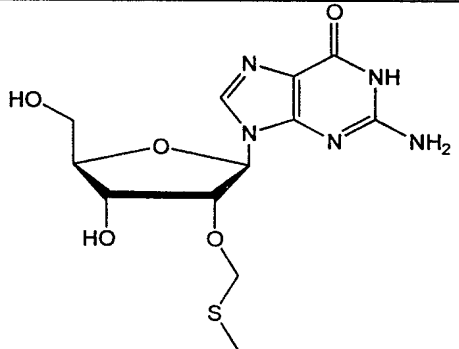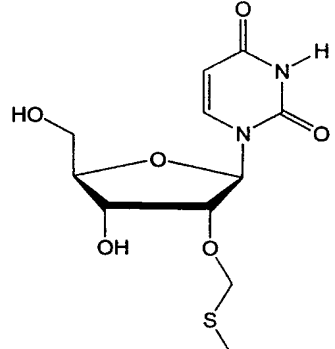
Thus, additional embodiments are within the scope of the invention and within the following claims

TABLE 1. NUCLEOSIDES USED FOR CHEMICAL SYNTHESIS OF MODIFIED NUCLEOTIDE TRIPHOSPHATES

	NUCLEOSIDES	ABBREVIATION	CHEMICAL STRUCTURE
1	2'-*O*-methyl-2,6-diaminopurine riboside	2'-*O*-Me-DAP	
2	2'-deoxy-2'amino-2,6-diaminopurine riboside	2'-NH$_2$-DAP	
3	2'-(*N*-alanyl)amino-2'-deoxy-uridine	ala-2'- NH$_2$ U	
4	2'-(*N*-phenylalanyl)amino-2'-deoxy-uridine	phe-2'-NH$_2$-U	

	NUCLEOSIDES	ABBREVIATION	CHEMICAL STRUCTURE
5	2'-(*N*-β-alanyl) amino-2'-deoxy uridine	2-β-Ala-NH₂-U	
6	2'-Deoxy-2'-(lysiyl) amino uridine	2'-L-lys-NH₂-U	
7	2'-C-allyl uridine	2'-C-allyl-U	
8	2'-*O*-amino-uridine	2'-*O*-NH₂-U	

	NUCLEOSIDES	ABBREVIATION	CHEMICAL STRUCTURE
9	2'-O-methylthiomethyl adenosine	2'-O-MTM-A	
10	2'-O-methylthiomethyl cytidine	2'-O-MTM-C	
11	2'-O-methylthiomethyl guanosine	2'-O-MTM-G	
12	2'-O-methylthiomethyl-uridine	2'-O-MTM-U	

	NUCLEOSIDES	ABBREVIATION	CHEMICAL STRUCTURE
13	2'-(*N*-histidyl) amino uridine	2'-his-NH$_2$-U	
14	2'-Deoxy-2'-amino-5-methyl cytidine	5-Me-2'-NH$_2$-C	
15	2'-(*N*-β-carboxamidine-β-alanyl)amino-2'-deoxy-uridine	β-ala-CA-NH$_2$-U	
16	2'-(*N*-β-alanyl) guanosine	β-Ala-NH$_2$-G	

	NUCLEOSIDES	ABBREVIATION	CHEMICAL STRUCTURE
17	2'-O-Amino-Adenosine	2'-O-NH$_2$-A	
18	2'-(N-lysyl)amino -2'-deoxy-cytidine	2'-NH$_2$-lys-C	
19	2'-Deoxy -2'-(L-histidine) amino Cytidine	2'-NH$_2$-his-C	
20	5-Imidazoleacetic acid 2'-deoxy-5'-triphosphate uridine	5-IAA-U	

TABLE 2. PHOSPHORYLATION OF URIDINE IN THE PRESENCE OF DMAP

0 equiv. DMAP		0.2 equiv. DMAP		0.5 equiv. DMAP		1.0 equiv. DMAP	
Time (min)	Product %	Time (min)	Product %	Time (min)	Product %	Time (min)	Product %
0	1	0	0	0	0	0	0
40	7	10	8	20	27	30	74
80	10	50	24	60	46	70	77
120	12	90	33	100	57	110	84
160	14	130	39	140	63	150	83
200	17	170	43	180	63	190	84
240	19	210	47	220	64	230	77
320	20	250	48	260	68	270	79
1130	48	290	49	300	64	310	77
1200	46	1140	68	1150	76	1160	72
		1210	69	1220	76	1230	74

TABLE 3. DETAILED DESCRIPTION OF THE NTP INCORPORATION REACTION CONDITIONS

Condition No.	TRIS-HCL (mM)	MgCl₂ (mM)	DTT (m M)	Spermidine (mM)	Triton X-100 (%)	METHANOL (%)	LiCl (mM)	PEG (%)	Temp (°C)
1	40 (pH 8.0)	20	10	5	0.01	10	1	-	25
2	40 (pH 8.0)	20	10	5	0.01	10	1	4	25
3	40 (pH 8.1)	12	5	1	0.002	-	-	4	25
4	40 (pH 8.1)	12	5	1	0.002	10	-	4	25
5	40 (pH 8.1)	12	5	1	0.002	-	1	4	25
6	40 (pH 8.1)	12	5	1	0.002	10	1	4	25
7	40 (pH 8.0)	20	10	5	0.01	10	1	-	37
8	40 (pH 8.0)	20	10	5	0.01	10	1	4	37
9	40 (pH 8.1)	12	5	1	0.002	-	-	4	37
10	40 (pH 8.1)	12	5	1	0.002	10	-	4	37
11	40 (pH 8.1)	12	5	1	0.002	-	1	4	37
12	40 (pH 8.1)	12	5	1	0.002	10	1	4	37

TABLE 4. INCORPORATION OF MODIFIED NUCLEOTIDE TRIPHOSPHATES

Modification	COND # 1	COND # 2	COND # 3	COND # 4	COND # 5	COND # 6	COND # 7	COND # 8	COND # 9	COND # 10	COND # 11	COND # 12
2'-NH$_2$-ATP	1	2	3	5	2	4	1	2	10	11	5	9
2'- NH$_2$-CTP	11	37	45	64	25	70	26	54	292	264	109	244
2'- NH$_2$-GTP	4	7	6	14	5	17	3	16	10	21	9	16
2'- NH$_2$-UTP	14	45	4	100	85	82	48	88	20	418	429	440
2'-dATP	9	3	19	23	9	24	6	3	84	70	28	51
2'-dCTP	1	10	43	46	35	47	27	127	204	212	230	235
2'-dGTP	6	10	9	15	9	12	8	34	38	122	31	46
2'-dTTP	9	9	14	18	13	18	8	15	116	114	59	130
2'-*O*-Me-ATP	0	0	0	0	0	0	1	1	2	2	2	2
2'-*O*-Me-CTP	no data compared to ribo; incorporates at low level											
2'-*O*-Me-GTP	4	3	4	4	4	4	2	4	4	5	4	5
2'-*O*-Me-UTP	55	52	39	38	41	48	55	71	93	103	81	77
2'-*O*-Me-DAP	4	4	3	4	4	5	4	3	4	5	5	5
2'- NH$_2$-DAP	0	0	1	1	1	1	1	0	0	0	0	0
ala-2'-NH$_2$-UTP	2	2	2	2	3	4	14	18	15	20	13	14
phe-2'-NH$_2$-UTP	8	12	7	7	8	8	4	10	6	6	10	6
2'-β NH$_2$-ala-UTP	65	48	25	17	21	21	220	223	265	300	275	248
2'-F-ATP	227	252	98	103	100	116	288	278	471	198	317	185
2'-F-GTP	39	44	17	30	17	26	172	130	375	447	377	438
2'-*C*-allyl-UTP	3	2	2	3	3	2	3	3	3	2	3	3
2'-*O*-NH$_2$-UTP	6	8	5	5	4	5	16	23	24	24	19	24
2'-*O*-MTM-ATP	0	1	0	0	0	0	1	0	0	0	0	0
2'-*O*-MTM-CTP	2	2	1	1	1	1	3	4	5	4	5	3
2'-*O*-MTM-GTP	6	1	1	3	1	2	0	1	1	3	1	4

TABLE 5. INCORPORATION OF MODIFIED NUCLEOTIDE TRIPHOSPHATES USING WILD TYPE BACTERIOPHAGE T7 POLYMERASE

Modification	label	% ribo control
2'-NH$_2$-GTP	ATP	4%
2'-dGTP	ATP	3%
2'-*O*-Me-GTP	ATP	3%
2'-F-GTP	ATP	4%
2'-*O*-MTM-GTP	ATP	3%
2'-NH$_2$-UTP	ATP	39%
2'-dTTP	ATP	5%
2'-*O*-Me-UTP	ATP	3%
ala-2'-NH$_2$-UTP	ATP	2%
phe-2'-NH$_2$-UTP	ATP	1%
2'-β-ala-NH$_2$-UTP	ATP	3%
2'-C-allyl-UTP	ATP	2%
2'-*O*-NH$_2$-UTP	ATP	1%
2'-*O*-MTM-UTP	ATP	64%
2'-NH$_2$-ATP	GTP	1%
2'-*O*-MTM-ATP	GTP	1%
2'-NH$_2$-CTP	GTP	59%
2'-dCTP	GTP	40%

55

TABLE 6a. INCORPORATION OF 2'-his-UTP AND MODIFIED CTP's

Modification	2'-his-UTP	rUTP
CTP	16.1	100
2'-amino-CTP	9.5*	232.7
2'-deoxy-CTP	9.6*	130.1
2'-OMe-CTP	1.9	6.2
2'-MTM-CTP	5.9	5.1
control	1.2	

TABLE 6b. INCORPORATION OF 2'-his-UTP, 2-amino CTP, AND MODIFIED ATP's

Modification	2'-his-UTP and 2'-amino-CTP	rUTP and rCTP
ATP	15.7	100
2'-amino-ATP	2.4	28.9
2'-deoxy-ATP	2.3	146.3
2'-OMe-ATP	2.7	15
2'-F-ATP	4	222.6
2'-MTM-ATP	4.7	15.3
2'-OMe-DAP	1.9	5.7
2'-amino-DAP	8.9*	9.6

Numbers shown are a percentage of incorporation compared to the all-RNA control.

*-Bold number indicates best observed rate of modified nucleotide triphosphate incorporation.

TABLE 7. INCORPORATION OF 2'-his-UTP, 2'-NH₂-CTP, 2'-NH₂-DAP, AND rGTP USING VARIOUS REACTION CONDITIONS

Conditions	compared to all rNTP
7	8.7*
8	7*
9	2.3
10	2.7
11	1.6
12	2.5

Numbers shown are a percentage of incorporation compared to the all-RNA control.

*-Two highest levels of incorporation contained both methanol and LiCl.

TABLE 8. SELECTION OF OLIGONUCLEOTIDES WITH RIBOZYME ACTIVITY

Pool	Generation	Time	Substrate Remaining(%)	Time	Substrate Remaining (%)
N60	0	4 hr	100.00	24 hr	100.98
N60	14	4 hr	99.67	24 hr	97.51
N60	15	4 hr	98.76	24 hr	96.76
N60	16	4 hr	97.09	24 hr	96.60
N60	17	4 hr	79.50	24 hr	64.01
N40	0	4 hr	99.89	24 hr	99.78
N40	10	4 hr	99.74	24 hr	99.42
N40	11	4 hr	97.18	24 hr	90.38
N40	12	4 hr	61.64	24 hr	44.54
N40	13	4 hr	54.28	24 hr	36.46
N20	0	4 hr	99.18	24 hr	100.00
N20	11	4 hr	100.00	24 hr	100.00
N20	12	4 hr	99.51	24 hr	100.00
N20	13	4 hr	90.63	24 hr	84.89
N20	14	4 hr	91.16	24 hr	85.92
N60B	0	4 hr	100.00	24 hr	100.00
N60B	1	4 hr	100.00	24 hr	100.00
N60B	2	4 hr	100.00	24 hr	100.00
N60B	3	4 hr	100.00	24 hr	100.00
N60B	4	4 hr	99.24	24 hr	100.00
N60B	5	4 hr	97.81	24 hr	96.65
N60B	6	4 hr	89.95	24 hr	77.14

TABLE 9. KINETIC ACTIVITY OF COMBINATORIAL LIBRARIES

Pool	Generation	k_{obs} (min^{-1})
N60	17	0.0372
	18	0.0953
	19	0.0827
N40	12	0.0474
	13	0.037
	14	0.065
	15	0.0254
N20	13	0.0359
	14	0.0597
	15	0.0549
	16	0.0477
N60B	6	0.0209
	7	0.0715
	8	0.0379

TABLE 10. KINETIC ACTIVITY OF CLONES WITHIN N60 AND N40 COMBINATORIAL LIBRARIES

clone	library	activity(min^{-1})	k_{rel}
G18	N60	0.00226	1.00
0-2	N60	0.0389	17.21
0-3	N60	0.000609	0.27
0-5	N60	0.000673	0.30
0-7	N60	0.00104	0.46
0-8	N60	0.000739	0.33
0-11	N60	0.0106	4.69
0-12	N60	0.00224	0.99
0-13	N60	0.0255	11.28
0-14	N60	0.000878	0.39
0-15	N60	0.0000686	0.03
0-21	N60	0.0109	4.82
0-22	N60	0.000835	0.37
0-24	N60	0.000658	0.29
0-28	N40	0.000741	0.33
0-35	N40	0.00658	2.91
3-1	N40	0.0264	11.68
3-3	N40	0.000451	0.20
7	N40	0.000854	0.38
3-15	N40	0.000832	0.37

TABLE 11. EFFECT OF MAGNESIUM CONCENTRATION OF THE CLEAVAGE RATE OF N20

$[Mg^{++}]$	$k_{obs}(min^{-1})$
25	0.0259
20	0.0223
15	0.0182
10	0.0208
5	0.0121
2	0.00319
2	0.00226

TABLE 12. CLASS I ENZYMATIC NUCLEIC ACID MOTIFS TARGETING HCV

Gene Name	Site	Chem Seq
HCV.R1A	6	ggagugucgc Ggaggaaacucc CU UCAAGGACAUCGUCCGGG cccau B
HCV.R1A	56	acgcuuucug GgaggaaacucC CU UCAAGGACAUCGUCCGGG gugaa B
HCV.R1A	75	auacuaacgc GgaggaaacucC CU UCAAGGACAUCGUCCGGG auggc B
HCV.R1A	76	cauacuaacg GgaggaaacucC CU UCAAGGACAUCGUCCGGG caugg B
HCV.R1A	95	cuggaggcug GgaggaaacucC CU UCAAGGACAUCGUCCGGG acgac B
HCV.R1A	138	accgguuccg GgaggaaacucC CU UCAAGGACAUCGUCCGGG agacc B
HCV.R1A	146	guguacucac GgaggaaacucC CU UCAAGGACAUCGUCCGGG gguuc B
HCV.R1A	158	cuggcaauuc GgaggaaacucC CU UCAAGGACAUCGUCCGGG ggugu B
HCV.R1A	164	gucguccugg GgaggaaacucC CU UCAAGGACAUCGUCCGGG aauuc B
HCV.R1A	176	agaaaggacc GgaggaaacucC CU UCAAGGACAUCGUCCGGG ggucg B
HCV.R1A	177	aagaaaggac GgaggaaacucC CU UCAAGGACAUCGUCCGGG cgguc B
HCV.R1A	209	cccaaaucuc GgaggaaacucC CU UCAAGGACAUCGUCCGGG aggca B
HCV.R1A	237	acucggcuag GgaggaaacucC CU UCAAGGACAUCGUCCGGG agucu B
HCV.R1A	254	uuucgcgacc GgaggaaacucC CU UCAAGGACAUCGUCCGGG aacac B
HCV.R1A	255	cuuucgcgac GgaggaaacucC CU UCAAGGACAUCGUCCGGG caaca B
HCV.R1A	259	aggccuuucg GgaggaaacucC CU UCAAGGACAUCGUCCGGG gaccc B
HCV.R1A	266	uaccacaagg GgaggaaacucC CU UCAAGGACAUCGUCCGGG cuuuc B
HCV.R1A	273	caggcaguac GgaggaaacucC CU UCAAGGACAUCGUCCGGG acaag B
HCV.R1A	288	ucgcaagcac GgaggaaacucC CU UCAAGGACAUCGUCCGGG cuauc B
HCV.R1A	291	cacucgcaag GgaggaaacucC CU UCAAGGACAUCGUCCGGG acccu B
HCV.R1A	7	uggagugucg GgaggaaacucC CU UCAAGGACAUCGUCCGGG cccca B
HCV.R1A	119	auggcucucc GgaggaaacucC CU UCAAGGACAUCGUCCGGG gggag B
HCV.R1A	120	uauggcucuc GgaggaaacucC CU UCAAGGACAUCGUCCGGG cggga B
HCV.R1A	133	uuccgcagac GgaggaaacucC CU UCAAGGACAUCGUCCGGG acuau B
HCV.R1A	140	ucaccgguuc GgaggaaacucC CU UCAAGGACAUCGUCCGGG gcaga B
HCV.R1A	188	cgggguuauc GgaggaaacucC CU UCAAGGACAUCGUCCGGG aagaa B
HCV.R1A	198	aggcauugag GgaggaaacucC CU UCAAGGACAUCGUCCGGG ggggu B
HCV.R1A	205	aaucuccagg GgaggaaacucC CU UCAAGGACAUCGUCCGGG auuga B
HCV.R1A	217	ggggcacgcc GgaggaaacucC CU UCAAGGACAUCGUCCGGG aaauc B
HCV.R1A	218	gggggcacgc GgaggaaacucC CU UCAAGGACAUCGUCCGGG caaau B
HCV.R1A	219	cgggggcacg GgaggaaacucC CU UCAAGGACAUCGUCCGGG ccaaa B
HCV.R1A	223	cuugcggggg GgaggaaacucC CU UCAAGGACAUCGUCCGGG acgcc B
HCV.R1A	229	agcagucuug GgaggaaacucC CU UCAAGGACAUCGUCCGGG ggggg B
HCV.R1A	279	cccuaucagg GgaggaaacucC CU UCAAGGACAUCGUCCGGG aguac B
HCV.R1A	295	ggggcacucg GgaggaaacucC CU UCAAGGACAUCGUCCGGG aagca B
HCV.R1A	301	ccucccgggg GgaggaaacucC CU UCAAGGACAUCGUCCGGG acucg B
HCV.R1A	306	cgagaccucc GgaggaaacucC CU UCAAGGACAUCGUCCGGG ggggc B
HCV.R1A	307	acgagaccuc GgaggaaacucC CU UCAAGGACAUCGUCCGGG cgggg B
No Ribo		GgaaaggugugcaaccggagucaucauaauggcuucCCUUCaaggaCaUCgCCg ggacggcB
Ribo		GGAAAGGUGUGCAACCGGAGUCAUCAUAAUGGCUCCCUUCAAGGACAUCGUC CGGGACGGCB

lower case = 2'Ome
U, C = 2'-amino-U, 2'-amino-C
G,A = ribo G,A
B = inverted abasic

TABLE 13. ADDITIONAL CLASS II ENZYMATIC NUCLEIC ACID MOTIFS

| Class II Motif ID	Sequence
A2	GGGAGGAGGAAGUGCCUGGUCAGUCACACCGAGACUGGCAGACGCUGAAACC GCCGCGCUCGCUCCCAGUCC
A12	GGGAGGAGGAAGUGCCUGGUAGUAAUAUAAUCGUUACUACGAGUGCAAGGUC GCCGCGCUCGCUCCCAGUCC
A11	GGGAGGAGGAAGUGCCUGGUAGUUGCCCGAACUGUGACUACGAGUGAGGUC GCCGCGCUCGCUCCCAGUCC
B14	GGGAGGAGGAAGUGCCUGGCGAUCAGAUGAGAUGAUGGCAGACGCAGAGACC GCCGCGCUCGCUCCCAGUCC
B10	GGGAGGAGGAAGUGCCUGGCGACUGAUACGAAAAGUCGCAGUUUCGAAACC GCCGCGCUCGCUCCCAGUCC
B21	GGGAGGAGGAAGUGCCUGGCGACUGAUACGAAAAGUCGCAGGUUUCGAAACC GCCGCGCUCGCUCCCAGUCC
B7	GGGAGGAGGAAGUGCCUUGGCUCAGCAUAAGUGAGCAGAUUGCGACACC GCCGCGCUCGCUCCCAGUCC
C8	GGGAGGAGGAAGUGCCUUGGUCAUUAGGAUGACAAACGUAUACUGAACACU GCCGCGCUCGCUCCCAGUCC

Claims:

1   An enzymatic nucleic acid molecule having formula II:
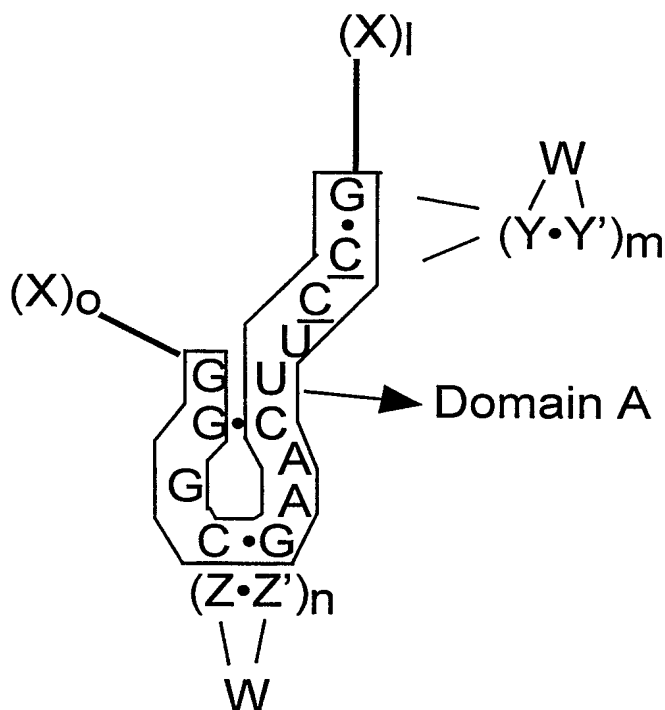
5   Wherein each X, Y, and Z represents independently a nucleotide which may be the same or different; l is an integer great than or equal to 3; m is an integer greater than 1 ; n is an integer greater than 1; 0 is an integer greater than or equal to 3; Z' is a nucleotide complementary to Z; Y' is a nucleotide complementary to Y; each X(l) and X(o) are oligonucleotides which are of sufficient length to stably interact
10   independently with a target nucleic acid sequence; W is a linker or ≥ 2 nucleotides; A, U, G, and C represent nucleotides; $\underline{C}$ is 2'-amino; and ___ represents a chemical linkage.

2   The nucleic acid of claim 1, wherein l is selected from the group consisting of 4, 5, 6, 7, 8, 9, 10, 11, 12, and 15.

64

3   The nucleic acid of claim 1, wherein m is selected from the group consisting of 2, 3, 4, 5, 6, and 7.

4   The nucleic acid of claim 1, wherein n is selected from the group consisting of 2, 3, 4, 5, 6, and 7.

5   The nucleic acid of claim 1, wherein o is selected from the group consisting of 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, and 15.

6   The nucleic acid of claim 1, wherein l and o are of the same length.

7   The nucleic acid of claim 1, wherein l and o are of different length.

8   The nucleic acid of claim 1, wherein the target nucleic acid sequence is selected from the group consisting of an RNA, DNA and RNA/DNA mixed polymer.

9   The nucleic acid of claim 1, wherein said chemical linkage is selected from the group consisting of phosphate ester linkage, amide linkage, phosphorothioate, and phosphorodithioate.

10   The nucleic acid of claim 1, wherein said $\underline{C}$ is selected from the group consisting of 2'-O-NH$_2$.

11   A method for inhibiting expression of a gene in a cell, comprising the step of administering to said cell the enzymatic nucleic acid molecule of claim 1 under conditions suitable for said inhibition.

12   A method of cleaving a separate RNA molecule comprising, contacting the enzymatic nucleic acid molecule of claim 1 with said separate RNA molecule under conditions suitable for the cleavage of said separate RNA molecule.

13   The method of claim 12, wherein said cleavage is carried out in the presence of a divalent cation.

14   The method of claim 12, wherein said divalent cation is Mg^{2+}.

15   The enzymatic nucleic acid molecule of claim 1, wherein said enzymatic nucleic acid molecule is chemically synthesized.

16   The enzymatic nucleic acid molecule of claim 1, wherein said enzymatic nucleic acid molecule comprises at least one ribonucleotide.

17   The enzymatic nucleic acid molecule of claim 1, wherein said enzymatic nucleic acid molecule comprises no ribonucleotide residues.

18   The enzymatic nucleic acid molecule of claim 1, wherein said enzymatic nucleic acid molecule comprises at least one 2-amino modification.

5   19   The enzymatic nucleic acid molecule of claim 1, wherein said enzymatic nucleic acid molecule comprises at least three phosphorothioate modifications.

20   The enzymatic nucleic acid molecule of claim 19, wherein said phosphorothioate modification is at the 5'-end of said enzymatic nucleic acid molecule.

21   The enzymatic nucleic acid molecule of claim 1, wherein said enzymatic
10   acid molecule comprises a 5'-cap or a 3'-cap or both a 5'-cap and a 3'-cap.

22   The enzymatic nucleic acid molecule of claim 21, wherein said 5-cap is phosphorothioate modification.

23   The enzymatic nucleic acid molecule of claim 21, wherein said 3'-cap is an inverted abasic moiety.

15 24. A compound having the formula I:
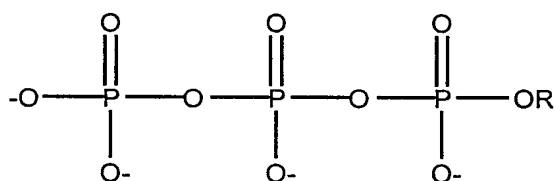
wherein R is independently any nucleoside selected from the group consisting of 2'-
O-methyl-2,6-diaminopurine   riboside;   2'-deoxy-2'amino-2,6-diaminopurine
riboside;   2'-(N-alanyl)   amino-2'-deoxy-uridine;   2'-(N-phenylalanyl)amino-2'-
20   deoxy-uridine; 2'-deoxy -2'-(N-β-alanyl) amino ; 2'-deoxy-2'-(lysiyl) amino uridine;
2'-C-allyl uridine; 2'-O-amino-uridine; 2'-O-methylthiomethyl adenosine; 2'-O-
methylthiomethyl   cytidine   ;   2'-O-methylthiomethyl   guanosine;   2'-O-
methylthiomethyl-uridine; 2'-Deoxy-2'-(N-histidyl) amino uridine; 2'-deoxy-2'-
amino-5-methyl cytidine; 2'-(N-β-carboxamidine-β-alanyl)amino-2'-deoxy-uridine;
25   2'-deoxy-2'-(N-β-alanyl)-guanosine; 2'-O-amino-adenosine; ; 2'-(N-lysyl)amino -2'-
deoxy-cytidine; 2'-Deoxy -2'-(L-histidine) amino cytidine; and 5-Imidazoleacetic
acid 2'-deoxy-5'-triphosphate uridine.

25. A process for incorporation of the compounds of claim 24 into an oligonucleotide comprising the step of contacting said compound with a mixture comprising a nucleic acid template, an RNA polymerase enzyme, and an enhancer of modified nucleotide triphosphate incorporation, under conditions suitable for the incorporation of said compound into said oligonucleotide.

26. The process of claim 25, wherein said RNA polymerase is a T7 RNA polymerase.

27. The process of claim 25, wherein said RNA polymerase is a mutant T7 RNA polymerase.

28. The process of claim 25, wherein said RNA polymerase is a SP6 RNA polymerase.

29. The process of claim 25, wherein said RNA polymerase is a mutant SP6 RNA polymerase.

30. The process of claim 25, wherein said RNA polymerase is a T3 RNA polymerase.

31. The process of claim 25, wherein said RNA polymerase is a mutant T3 RNA polymerase.

32 The process of claim 25, wherein said enhancer of modified nucleotide triphosphate incorporation is selected from the group consisiting of LiCl, methanol, polyethylene glycol, diethyl ether, propanol, methylamine, and ethanol.

33. A process for the synthesis of a pyrimidine nucleotide triphosphate comprising the steps of:

(a) monophosphorylation, wherein a pyrimidine nucleoside is contacted with a mixture comprising a phosphorylating reagent, a trialkyl phosphate and dimethylaminopyridine, under conditions suitable for the formation of a pyrimidine nucleotide monophosphate; and

(b) pyrophosphorylation, wherein said pyrimidine monophosphate from step (a) is contacted with a pyrophosphorylating reagent under conditions suitable for the formation of said pyrimidine nucleotide triphosphate.

34. The process of claim 33, wherein said pyrimidine nucleoside triphosphate is uridine triphosphate.

35. The process of claim 33, wherein said uridine triphosphate has a 2'-sugar modification.

36. The process of claim 35, wherein said uridine triphosphate is 2'-*O*-methylthiomethyl uridine triphosphate.

37. The process of claim 33, wherein said phosphorylating agent is selected from the group consisting of phosphorus oxychloride, phospho-tris-triazolides and phospho-tris-triimidazolides.

38. A process of claim 33, wherein said trialkylphosphate is triethyl phosphate.

39. The process of claim 33, wherein said pyrophosphorylating reagent is tributyl ammonium pyrophosphate.

40. The process of claim 25, wherein said oligonucleotide is RNA.

41. The process of claim 25, wherein said oligonucleotide is an enzymatic nucleic acid molecule.

42. The process of claim 25, wherein said oligonucleotide is an aptamer.

43. A kit for synthesis of an oligonucleotide comprising an RNA polymerase, an enhancer of modified nucleotide triphosphate incorporation and at least one compound of claim 24.

44. A kit for synthesis of an oligonucleotide comprising a DNA polymerase, an enhancer of modified nucleotide triphosphate incorporation and at least one compound of claim 24.

45. The kit of claim 43, wherein said RNA polymerase is a bacteriophage T7 RNA polymerase.

46. The kit of claim 43, wherein said RNA polymerase is a bacteriophage SP6 RNA polymerase.

47. The kit of claim 43, wherein said RNA polymerase is a bacteriophage T3 RNA polymerase.

48. The kit of claim 43, wherein said RNA polymerase is a mutant T7 RNA polymerase.

49. The kit of claim 43 or 44, wherein said kit comprises at least two compounds of claim 24.

50. A nucleic acid catalyst comprising a histidyl modification, wherein said nucleic acid catalyst is able to catalyze an endonuclease reaction in the absence of a metal ion co-
5   factor.

51. The nucleic acid of claim 50, wherein said catalyst is able to cleave a separate nucleic acid molecule.

52. The nucleic acid of claim 51, wherein said separate nucleic acid molecule is an RNA molecule.

1053. The nucleic acid of claim 51, wherein said separate nucleic acid molecule is an DNA molecule.

54. The nucleic acid catalyst of claim 50, wherein said nucleic acid catalyst comprises at least one ribonucleotide.
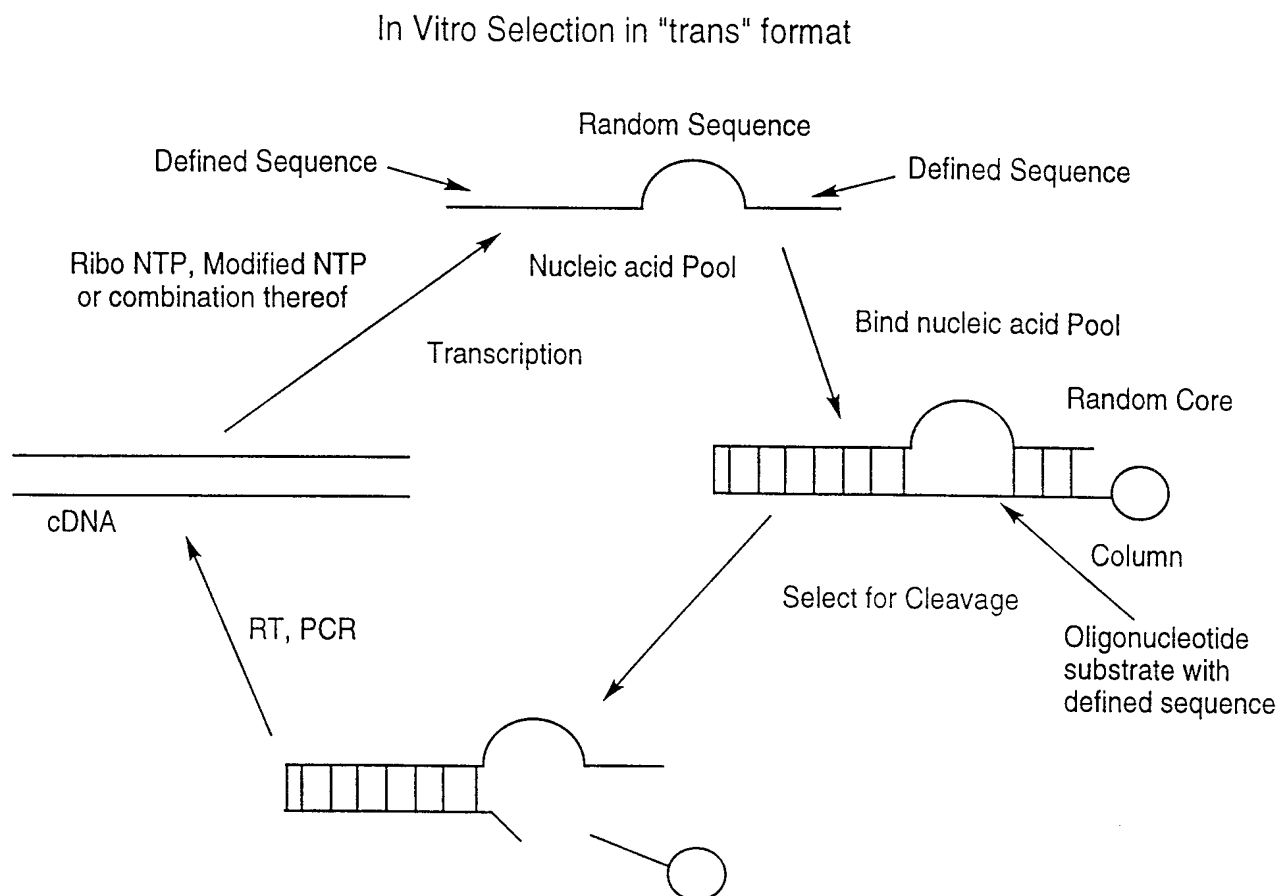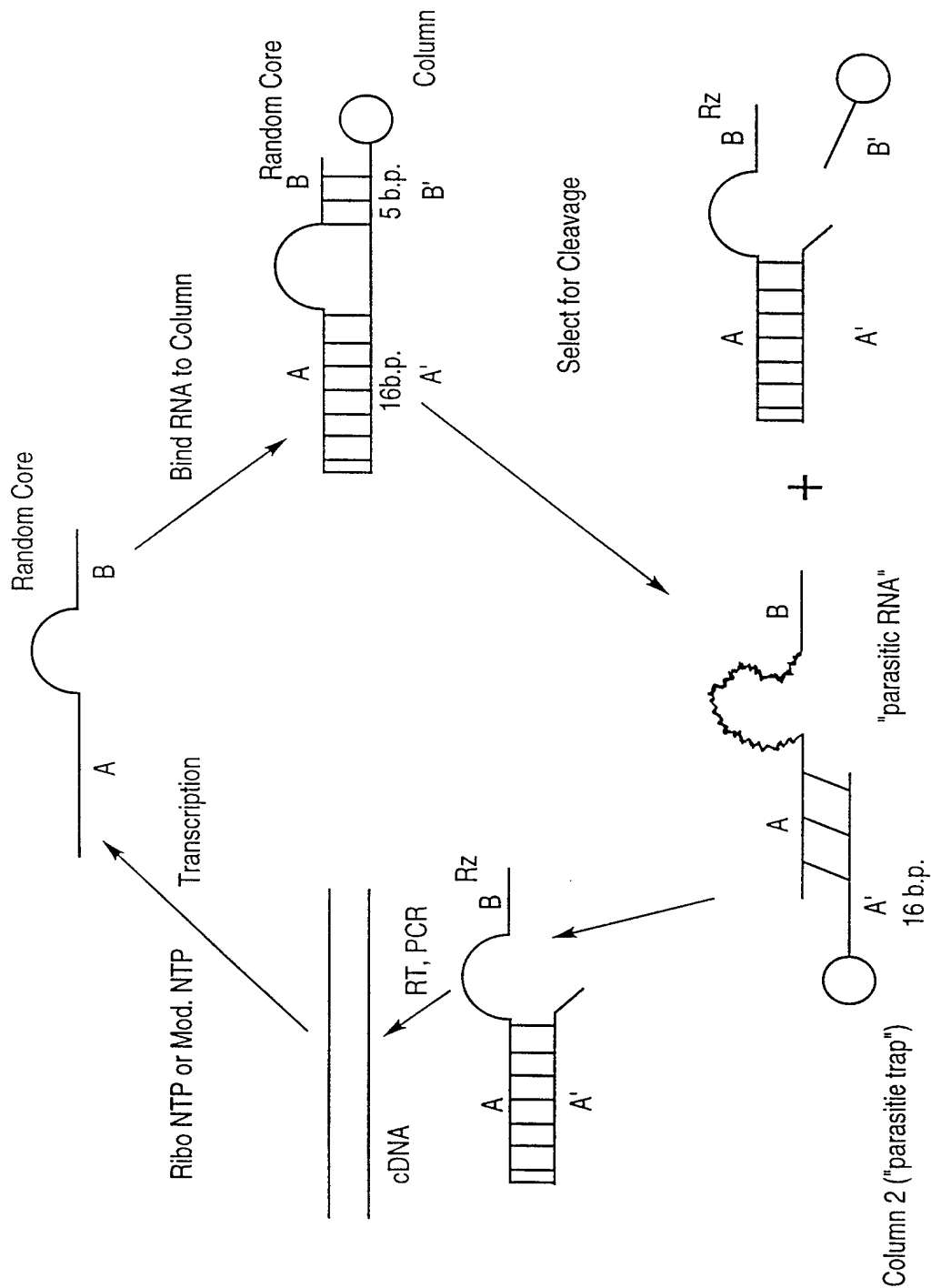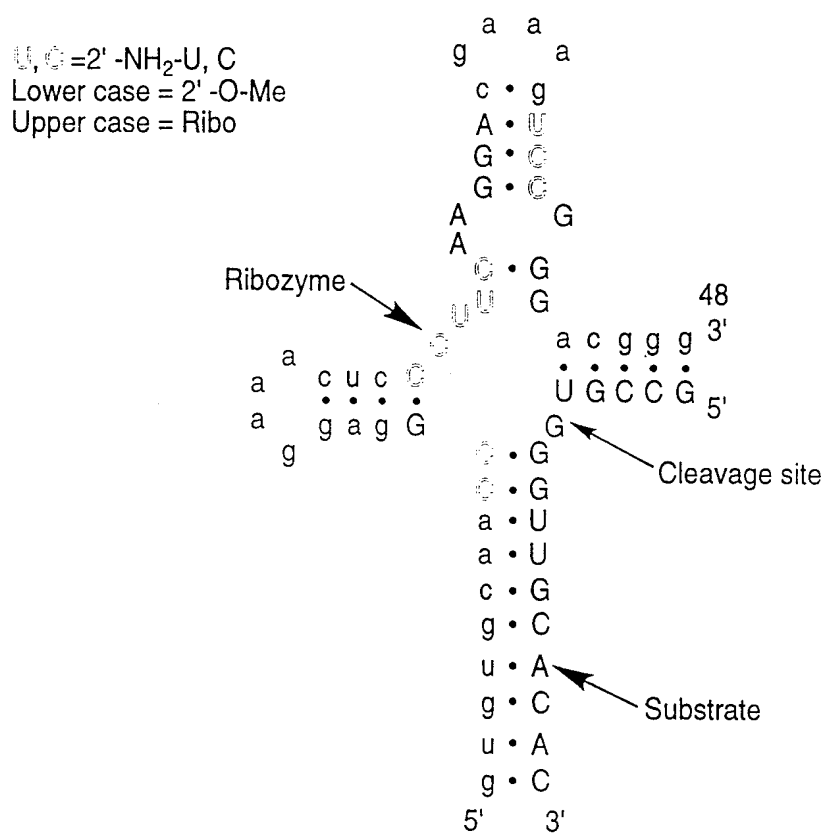
15

FIG. 1.

In Vitro Selection in "trans" format

FIG. 2.

FIG. 3.

U, C = 2'-NH₂-U, C
Lower case = 2'-O-Me
Upper case = Ribo

```
                         a   a
                       g       a
                       c • g
                       A • U
                       G • C
                       G • C
                     A       G
                     A
         Ribozyme    C • G
                   U U   G             48
                                        3'
              a                 a c g g g
            a   c u c C         • • • • •
          a   • • •   •         U G C C G  5'
            a g a g G           G
              g                         Cleavage site
                       C • G
                       C • G
                       a • U
                       a • U
                       c • G
                       g • C
                       u • A
                       g • C         Substrate
                       u • A
                       g • C
                     5'       3'
```
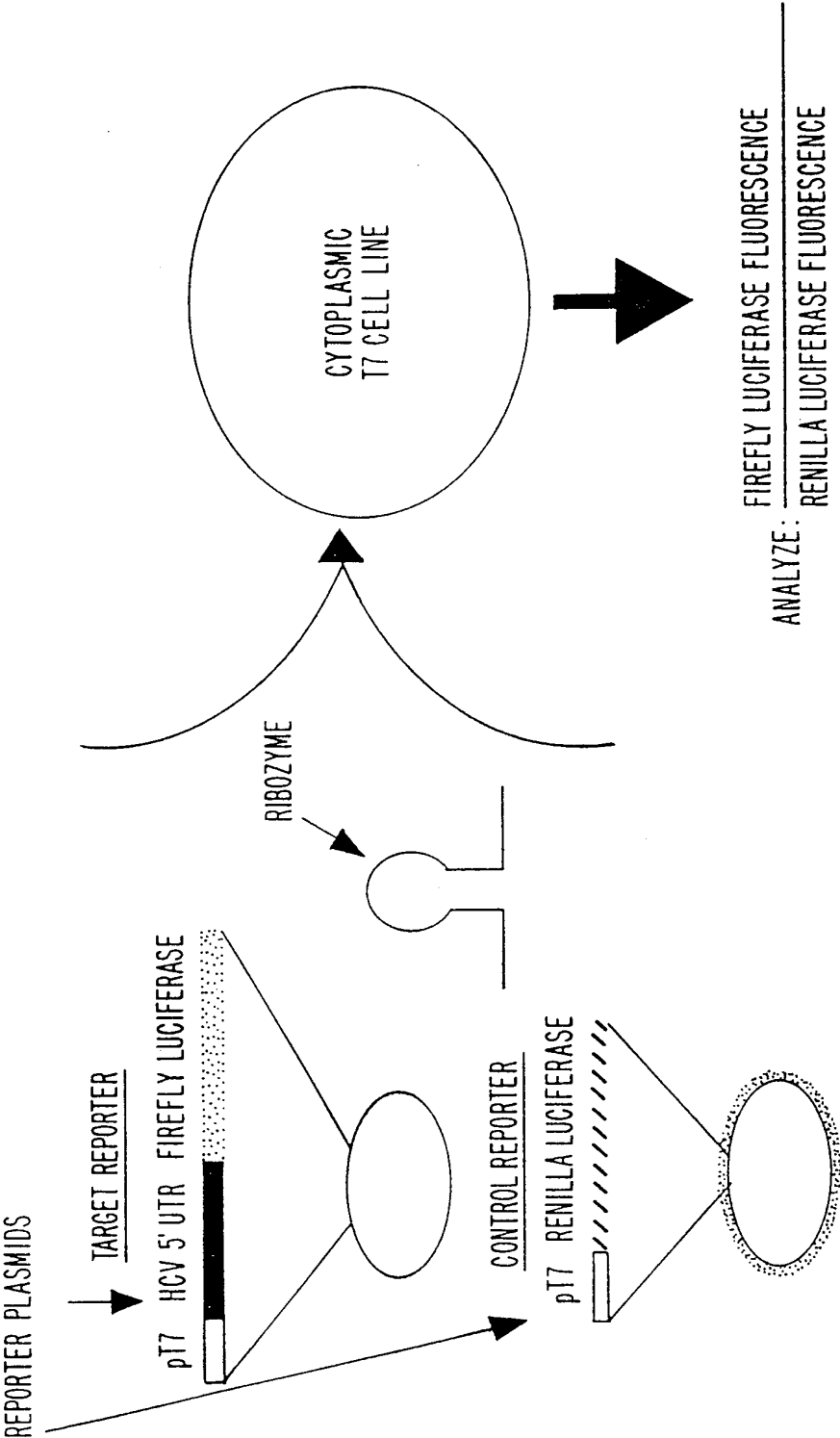
FIG. 4.

FIG. 5.

FIG. 6.

FIG. 7.

FIG. 8.

	Rate (min⁻¹)	Required NTP
	(Suboptimal)	
A1	0.05	2'-NH₂-CTP
A5	0.03	2'-NH₂-CTP
B2	0.11	2'-NH₂-CTP
B6	0.1	2'-NH₂-CTP
B23	0.05	2'-NH₂-CTP
C5	0.01	2'-NH₂-CTP